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OM protein - protein search, using sw model

Run on: January 30, 2003, 13:31:57 ; Search time 35 Seconds
(without alignments)
38.072 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLSGEPQC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	10	22 AAB46753	MMP-9 antagonist p
2	45	76.3	10	22 AAB46754	MMP-9 antagonist p
3	42	71.2	2091	22 ABB70224	Drosophila melanog
4	41	69.5	798	22 AAB39360	Human polypeptide
5	41	69.5	798	22 AAB36937	Human integrin bet
6	41	69.5	805	22 AA411146	Human polypeptide
7	41	69.5	963	19 AA470540	Integrin beta-1 ch
8	40	67.8	62	22 ASG29623	Novel human diagno
9	40	67.8	145	22 ABB21707	Novel human diagno
10	40	67.8	191	22 ABB21688	Novel human diagno

11	40	67.8	205	22 ABB21679	Novel human diagno
12	40	67.8	207	22 ABB21676	Novel human diagno
13	40	67.8	247	22 ABB21675	Novel human diagno
14	40	67.8	257	22 ABB21680	Novel human diagno
15	40	67.8	1043	22 ABB06467	Novel human diagno
16	39	66.1	10	22 AAB46755	MMP-9 antagonist p
17	39	66.1	110	22 AAB38902	Human polypeptide
18	39	66.1	179	12 AAR15426	Bovine epithelin p
19	39	66.1	228	22 AAM40688	Human polypeptide
20	38.5	65.3	163	22 AAW88487	Human ribonuclease
21	38	64.4	17	21 AAB52042	Human secreted pro
22	38	64.4	157	22 ABB70321	Drosophila melanog
23	38	64.4	230	22 ABB25277	Novel human diagno
24	38	64.4	345	21 AAB01456	PML mutant polypep
25	38	64.4	358	11 AAR05123	Bat-PA(L). Desmod
26	38	64.4	367	21 AAB01455	PML mutant polypep
27	38	64.4	394	11 AAR06486	v-PA.gamma. Desmo
28	38	64.4	395	11 AAR05125	Modified Bat-PA(H)
29	38	64.4	431	11 AAR06459	v-PA.beta. Desmod
30	38	64.4	477	11 AAR05122	Bat-PA(H). Desmod
31	38	64.4	477	11 AAR05122	Bat-PA(H). Desmod
32	38	64.4	560	13 AAR27535	myl protein. Synt
33	38	64.4	560	20 AAW81965	Human myl-1 protel
34	38	64.4	797	13 AAR27533	myl/RAR-alpha fusi
35	38	64.4	797	20 AAW81963	Human myl/RAR-alpha
36	38	64.4	798	23 ABB57079	Mouse ischaemic co
37	38	64.4	819	22 ABB18860	Novel human diagno
38	37	62.7	71	20 AAY05202	Human FCMF follist
39	37	62.7	159	22 AAM87880	Human immune/haema
40	37	62.7	206	21 AAB32113	Human secreted pro
41	37	62.7	263	20 AAY14571	Human apoptosis in
42	37	62.7	263	20 AAY06201	Follistatin module
43	37	62.7	263	20 AAY01098	Human follistatin-
44	37	62.7	263	22 AAU12413	Human PRO1308 poly
45	37	62.7	263	22 AAY72875	Human PRO1308 prot

ALIGNMENTS

RESULT 1
AAB46753
ID AAB46753 standard; peptide; 10 AA.
XX AAB46753;
AC
XX
XX
DT 12-APR-2001 (first entry)
XX
DE MMP-9 antagonist peptide FRIP-1.
XX
KW Antagonist; MMP-9; inhibition; angiogenesis; tumor growth; beta-integrin;
KW protein-protein interaction; matrix metalloproteinase; cytosolic; sarcoma;
KW antitumor; antiproliferative; vasotropic; antidiabetic; osteopathic; glioma;
KW anti-rheumatoid; antiarthritic; antiatherosclerotic; ophthalmological;
KW antiinflammatory; metastasis; psoriasis; macular degeneration;
KW neurological disease; testis; melanoma; carcinoma; fibrosarcoma;
KW astrocytoma; diabetic retinopathy; neovascular glaucoma; osteoporosis;
KW atherosclerotic plaques; rheumatoid arthritis.
OS Synthetic.
XX
XX WO200104157-A2.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US19095.
XX
PR 13-JUL-1999; 99US-0143581.
XX
PR 02-SEP-1999; 99US-0152495.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Brooks PC, Hassanieh L, Rodriguez D;

XX DR WPI; 2001-138319/14.

XX PF Novel antagonist inhibiting angiogenesis by modifying protein-protein

XX PT interactions, specifically matrix metalloproteinase-9 - beta1 containing

XX PT integrin interaction, useful to inhibit psoriasis, macular degeneration

XX PT

XX PS Claim 27; Page 60; 61pp; English.

XX CC This invention describes a novel antagonist (I) that inhibits

XX CC angiogenesis and/or tumor growth by modifying protein-protein

XX CC interactions which specifically binds to matrix metalloproteinase (MMP)-9

XX CC or beta-1 integrin. The products of the invention have cytostatic,

XX CC antitumor, antipsoriatic, vasotropic, antidiabetic, osteopathic,

XX CC anti-rheumatoid, antiarthritic, antiatherosclerotic, ophthalmological and

XX CC antiinflammatory activity. (I) inhibits angiogenesis, tumor growth,

XX CC neurological disease, or restenosis in a tissue. (I) is useful for

XX CC inhibiting angiogenesis, in a mammalian arthritic, ocular, retinal, or

XX CC hemangioma tissue which is inflamed and angiogenesis is occurring. (I) is

XX CC also useful for inhibiting tumor growth or metastasis such as melanoma,

XX CC carcinoma, sarcoma, fibrosarcoma, glioma, or astrocytoma, in a tissue.

XX CC (I) is also useful for inhibiting psoriasis, macular degeneration or

XX CC restenosis in a tissue. In all the above conditions, (I) is administered

XX CC in conjunction with chemotherapy or radiation. (I) is also useful for

XX CC detecting angiogenesis and detecting tumors or tumor invasion in a tissue

XX CC ex vivo. The antagonist in this case is conjugated to fluorochrome,

XX CC radioactive tag, paramagnetic heavy metal, diagnostic dye or enzyme. (I)

XX CC is also useful for inhibiting psoriasis, macular degeneration, or

XX CC atherosclerotic plaques, osteoporosis, rheumatoid arthritis and other

XX CC inflammatory diseases. The method are effective in part because the

XX CC therapy is highly selective for angiogenesis and no other biological

XX CC processes. Only new vessel growth is inhibited by antagonists that

XX CC disrupt the localization of MMP-9, and therefore the therapeutic methods

XX CC do not adversely effect mature vessels. Also, because certain of (I)

XX CC affect only the localization of MMP-9, and do not directly block the

XX CC proteolytic activity of MMP-9 or the adhesive functions of the beta1

XX CC integrins, it is likely that these compounds will have fewer side effects

XX CC because the proteolytic activity of MMP-9 or the adhesive functions of

XX CC the beta1 integrins may have normal physiological functions. The

XX CC antagonists are highly potent suggesting that they may have therapeutic

XX CC benefits at low concentrations.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 59; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CRLRSGEPQC 10

Db |||||

1 CRLRSGEPQC 10

RESULT 2

AAB46754

ID AAB46754 standard; peptide; 10 AA.

XX AC AAB46754;

XX DT

XX DT 12-APR-2001 (first entry)

XX DE MMP-9 antagonist peptide AAA.

XX KW Antagonist: MMP-9; inhibition; angiogenesis; tumor growth; beta-integrin;

XX KW protein-protein interaction; matrix metalloproteinase; cytostatic; sarcoma;

XX KW antitumor; antipsoriatic; vasotropic; antidiabetic; osteopathic; glioma;

XX KW anti-rheumatoid; antiarthritic; antiatherosclerotic; ophthalmological;

XX KW antiinflammatory; metastasis; psoriasis; macular degeneration;

XX KW neurological disease; restenosis; melanoma; carcinoma; fibrosarcoma;

XX KW astrocytoma; diabetic retinopathy; neovascular glaucoma; osteoporosis;

XX KW atherosclerotic plaques; rheumatoid arthritis.

XX SS Synthetic.

XX PN WO200104157-A2.

XX XX

XX PD 18-JAN-2001.

XX XX

XX PF 13-JUL-2000; 2000WO-US19095.

XX XX

XX PR 13-JUL-1999; 99US-0143581.

XX PR 02-SEP-1999; 99US-0152495.

XX XX

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX XX

XX PI Brooks PC, Hassanieh L, Rodriguez D;

XX DR WPI; 2001-138319/14.

XX CC Novel antagonist inhibiting angiogenesis by modifying protein-protein

XX CC interactions, specifically matrix metalloproteinase-9 - beta1 containing

XX CC integrin interaction, useful to inhibit psoriasis, macular degeneration

XX CC

XX PS Example 7; Page 60; 61pp; English.

XX CC This invention describes a novel antagonist (I) that inhibits

XX CC angiogenesis and/or tumor growth by modifying protein-protein

XX CC interactions which specifically binds to matrix metalloproteinase (MMP)-9

XX CC or beta-1 integrin. The products of the invention have cytostatic,

XX CC antitumor, antipsoriatic, vasotropic, antidiabetic, osteopathic,

XX CC anti-rheumatoid, antiarthritic, antiatherosclerotic, ophthalmological and

XX CC antiinflammatory activity. (I) inhibits angiogenesis, tumor growth,

XX CC metastasis, or a disease state such as psoriasis, macular degeneration,

XX CC neurological disease, or restenosis in a tissue. (I) is useful for

XX CC inhibiting angiogenesis, in a mammalian arthritic, ocular, retinal, or

XX CC hemangioma tissue which is inflamed and angiogenesis is occurring. (I) is

XX CC also useful for inhibiting tumor growth or metastasis such as melanoma,

XX CC carcinoma, sarcoma, fibrosarcoma, glioma, or astrocytoma, in a tissue.

XX CC (I) is also useful for inhibiting psoriasis, macular degeneration or

XX CC restenosis in a tissue. In all the above conditions, (I) is administered

XX CC in conjunction with chemotherapy or radiation. (I) is also useful for

XX CC detecting angiogenesis and detecting tumors or tumor invasion in a tissue

XX CC ex vivo. The antagonist in this case is conjugated to fluorochrome,

XX CC radioactive tag, paramagnetic heavy metal, diagnostic dye or enzyme. (I)

XX CC is also useful for treating diabetic retinopathy, neovascular glaucoma,

XX CC atherosclerotic plaques, osteoporosis, rheumatoid arthritis and other

XX CC inflammatory diseases. The method are effective in part because the

XX CC therapy is highly selective for angiogenesis and no other biological

XX CC processes. Only new vessel growth is inhibited by antagonists that

XX CC disrupt the localization of MMP-9, and therefore the therapeutic methods

XX CC do not adversely effect mature vessels. Also, because certain of (I)

XX CC affect only the localization of MMP-9, and do not directly block the

XX CC proteolytic activity of MMP-9 or the adhesive functions of the beta1

XX CC integrins, it is likely that these compounds will have fewer side effects

XX CC because the proteolytic activity of MMP-9 or the adhesive functions of

XX CC the beta1 integrins may have normal physiological functions. The

XX CC antagonists are highly potent suggesting that they may have therapeutic

XX CC benefits at low concentrations.

XX SQ Sequence 10 AA;

Query Match 76.3%; Score 45; DB 22; Length 10;

Best Local Similarity 70.0%; Pred. No. 0.57;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CRLRSGEPQC 10

Db |||||

1 CRLRSGEPQC 10

RESULT 3

ABB70224

ID ABB70224 standard; Protein; 2091 AA.

```

XX AC ABB70224;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 37464.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX PI WPI; 2001-656860/75.
XX DR N-PSDB; ABL14327.
XX DR
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX PS Disclosure; SEQ ID NO 37464; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins
XX CC (ABB57737-ABB72072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 2091 AA;
XX Query Match 71.2%; Score 42; DB 22; Length 2091;
XX Best Local Similarity 88.9%; Pred. No. 2.3e+02;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 CRLRSGEPQ 9
XX Db 1632 CRLRSGEAQ 1640
XX RESULT 4
XX AAM39360
XX ID AAM39360 standard; Protein; 798 AA.
XX AC AAM39360;
XX XX
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 2505.
XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX KW peripheral nervous system; neuropathy; central nervous system; CNS;
XX KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX KW leukaemia.
XX OS Homo sapiens.
XX OS WO200153312-A1.
XX PN 26-JUL-2001.
XX PD
XX PF 26-DEC-2000; 2000WO-US34263.
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX DR WPI; 2001-442253/47.
XX DR N-PSDB; AAI58516.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries.
XX XX
XX PS Example 4; SEQ ID NO 2505; 10078pp; English.
XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
XX CC the encoded polypeptides (AAM3642-AAW42213) with nootropic,
XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC C.N.S disorders.
XX CC Note: the sequence data for this patent did not form part of the printed
XX CC specification.
XX SQ Sequence 798 AA;
XX Query Match 69.5%; Score 41; DB 22; Length 798;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 2 RLRSGEQP 9
XX Db 122 RLRSGEQP 129
XX RESULT 5
XX AAB36937
XX ID AAB36937 standard; protein; 798 AA.
XX AC AAB36937;
XX XX
XX DT 27-FEB-2001 (first entry)
XX DE Human integrin beta 1 subunit.
XX KW Tenascin-C; axon; dendrite; neurite.
XX KW Homo sapiens.

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XX WO2000066628-A1.
XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US11647.
XX 01-MAY-1999; 99US-0132137.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Geller HM, Meiners S;
XX WPI; 2001-015974/02.
XX New peptides and methods of stimulating axonal and/or dendritic growth
XX and/or guidance by administering a peptide, particularly comprising a
XX tenascin-C region, to a neuron -
XX Disclosure; Page 20; 73pp; English.
XX The present invention relates to a tenascin-C peptide. The peptide,
XX particularly from a tenascin-C region, is used for stimulating axonal
XX and/or dendritic growth, independent of neurite guidance, and
XX stimulating axonal and/or dendritic guidance independent of axonal
XX and/or dendritic growth.
XX Sequence 798 AA;
SQ
Query Match 69.5%; Score 41; DB 22; Length 798;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RLRSGEPQ 9
DB 122 RLRSGEPQ 129
RESULT 6
AAM41146
ID AAM41146 standard; Protein; 805 AA.
XX AAM41146;
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 6077.
XX
KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX WO200153312-A1.
XX 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US34263.
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-052317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX (HYSE-) HYSEQ INC.
PA

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
XX N-PSDB; AAI60302.
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX Example 2; SEQ ID NO 6077; 10078pp; English.
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
XX the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity; cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
XX Sequence 805 AA;
SQ
Query Match 69.5%; Score 41; DB 22; Length 805;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RLRSGEPQ 9
DB 126 RLRSGEPQ 133
RESULT 7
AAW70540
ID AAW70540 standard; Protein; 963 AA.
XX AAW70540;
XX 26-JAN-1999 (first entry)
DE Integrin beta-1 chain.
XX
KW Integrin; beta-1 chain; immunoglobulin; chimeric; heterodimer complex;
KW inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic agent;
KW human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /note= "signal peptide"
FT /note= "mature protein"
XX WO9832771-A1.
XX 30-JUL-1998.
XX 29-JAN-1998; 98WO-JP00370.
XX 29-AUG-1997; 97JP-0234544.
XX 29-JAN-1997; 97JP-0015118.
XX (TORA ) TORAY IND INC.
PA

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XX Kainoh M, Tanaka T;
 XX WPI; 1998-427881/36.
 DR N-PSDB; AAV33773.
 XX
 XX Integrin-immunoglobulin chimeric protein heterodimer complexes as
 PT platelet substitutes - contain the alpha and beta integrin chains
 PT associated in stable state and bind to extracellular matrix in the
 PT presence of plasma components
 XX
 XX Claim 9; Pages 50-57; 87pp; Japanese.
 XX
 XX This represents an integrin beta-1 chain. The invention provides
 CC integrin-immunoglobulin chimeric protein heterodimer complexes that
 CC comprise an integrin alpha or beta chain associated with an
 CC immunoglobulin light or heavy chain. These chimeric proteins form
 CC heterodimer complexes, in particular with a chimeric protein containing
 CC an integrin alpha chain and an immunoglobulin chain with a chimeric
 CC protein containing an integrin beta chain and an immunoglobulin chain;
 CC the immunoglobulin chain in each case may be a heavy chain, or one of the
 CC two may be a light chain. The integrin alpha chain is preferably alpha 4
 CC or alpha 2 and the integrin beta chain is preferably beta 1. Animal cells
 CC transformed with vectors containing the DNA coding for the above chimeric
 CC proteins can be used in the preparation of the chimeric proteins and
 CC their heterodimer complexes. The heterodimer complexes, which are useful
 CC for testing potential promoters and inhibitors of the binding of
 CC integrins to their ligands, function as blood platelet substitutes and
 CC hemostatics and as diagnostic agents.
 XX
 XX Sequence 963 AA;
 SQ
 Query Match 69.5%; Score 41; DB 19; Length 963;
 Best Local Similarity 100.0%; Pred. No. 1.6e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RLRSGEPPQ 9
 Db 122 RLRSGEPPQ 129
 |||||
 RESULT 8
 ABG29623
 ID ABG29623 standard; Protein; 62 AA.
 XX
 XX AC ABG29623;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #29614.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 XX Homo sapiens.
 OS
 XX WO200175067-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US08631.
 PF
 XX 31-MAR-2000; 2000US-0540217.
 PR
 XX 23-AUG-2000; 2000US-0649167.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR
 XX N-PSDB; AAS93810.
 DR
 XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 XX Claim 20; SEQ ID No 59982; 103pp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 62 AA;
 SQ
 Query Match 67.8%; Score 40; DB 22; Length 62;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRLRSGEPQ 9
 Db 2 CRLRAGDPR 10
 |||||
 RESULT 9
 ABG21707
 ID ABG21707 standard; Protein; 145 AA.
 XX
 XX AC ABG21707;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #21698.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 XX Homo sapiens.
 OS
 XX WO200175067-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US08631.
 PF
 XX 31-MAR-2000; 2000US-0540217.
 PR
 XX 23-AUG-2000; 2000US-0649167.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR
 XX N-PSDB; AAS85894.
 DR
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess

PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 52066; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 145 AA;
 Query Match 67.8%; Score 40; DB 22; Length 145;
 Best Local Similarity 70.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CRLRSGEPOC 10
 II IIII I
 Db 96 CRARSGEEXC 105
 RESULT 10
 ABG21688
 ID ABG21688 standard; Protein; 191 AA.
 XX
 AC ABG21688;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #21679.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS85875.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX

PS Claim 20; SEQ ID No 52047; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 191 AA;
 Query Match 67.8%; Score 40; DB 22; Length 191;
 Best Local Similarity 70.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CRLRSGEPOC 10
 II IIII I
 Db 78 CRARSGEEXC 87
 RESULT 11
 ABG21679
 ID ABG21679 standard; Protein; 205 AA.
 XX
 AC ABG21679;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #21670.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS85866.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 52038; 103pp; English.

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG3377 represent novel human
CC amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

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Query Match          67.8%; Score 40; DB 22; Length 207;
Best Local Similarity 70.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db	96	CRARSGE	XC	105

RESULT 13
ABG21675
ID ABG21675 standard; Protein; 247 AA;

XX ABG21675;

DT 18-FEB-2002 (first entry)

XX
DE
Novel human diagnostic protein #21666.

AA
KW
KW
KW

YY Homo sapiens.

AA WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX
PR 31-MAR-2000: 2000US-0540217

PR 23-AUG-2000; 2000US-0649167.
XX

PA (HYSE-) HYSEQ INC.
YY

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

XX
N-ESDB, RA30300Z.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 20; SEQ ID No 52034; 103pp: English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (ii) sequences. (i) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (ii). The

CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 247 AA;
 SQ Query Match 67.8%; Score 40; DB 22; Length 247;
 Best Local Similarity 70.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRLRSGEQC 10
 || |||||
 Db 134 CRARSGEEXC 143

RESULT 14
 ABG21680
 ID ABG21680 standard; Protein; 257 AA.

AC ABG21680;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #21671.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR N-PSDB; AAS85867.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 20; SEQ ID No 52039; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 257 AA;

Query Match 67.8%; Score 40; DB 22; Length 257;
 Best Local Similarity 70.0%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRLRSGEQC 10
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 Db 144 CRARSGEEXC 153

RESULT 15

ABG06467

ID ABG06467 standard; Protein; 1043 AA.

AC ABG06467;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #6458.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR N-PSDB; AAS70654.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 20; SEQ ID No 36826; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (ii) and its binding partners are useful in medical
 CC imaging of sites expressing (ii). (i) and (ii) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 1043 AA;

Query Match 67.8%; Score 40; DB 22; Length 1043;

Best Local Similarity 70.0%; Pred. No. 2.6e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQC 10

||| ||| |

Db 1022 CRLHSGEKPC 1031

Search completed: January 30, 2003, 13:32:58

Job time : 36 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 30, 2003, 13:32:01 ; Search time 15 seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLRSGEPQC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*
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5: /cgn2.6/ptodata/1/iaa/PCRUS_COMB.pep.*
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	69.5	798	US-07-728-215-30	Sequence 30, Appl
2	41	69.5	798	US-08-938-085A-30	Sequence 30, Appl
3	39	66.1	179	US-07-668-648-8	Sequence 8, Appl
4	39	66.1	179	US-08-429-998-8	Sequence 8, Appl
5	39	66.1	179	US-08-431-333-8	Sequence 8, Appl
6	39	66.1	179	PCR-US91-02321-8	Sequence 8, Appl
7	38.5	65.3	150	US-08-867-676-3	Sequence 8, Appl
8	38.5	65.3	163	US-08-867-676-1	Sequence 3, Appl
9	38	64.4	477	US-08-560-098A-51	Sequence 51, Appl
10	38	64.4	560	US-08-095-728B-6	Sequence 6, Appl
11	38	64.4	560	PCR-US92-02320A-6	Sequence 6, Appl
12	38	64.4	797	US-08-095-728B-2	Sequence 2, Appl
13	38	64.4	797	PCR-US92-02320A-2	Sequence 2, Appl
14	37	62.7	71	US-08-972-008-4	Sequence 4, Appl
15	37	62.7	71	US-09-267-409-4	Sequence 4, Appl
16	37	62.7	263	US-08-972-008-2	Sequence 2, Appl
17	37	62.7	263	US-09-141-027-2	Sequence 2, Appl
18	37	62.7	263	US-09-267-409-2	Sequence 2, Appl
19	36	61.0	472	US-08-272-255-10	Sequence 10, Appl
20	36	61.0	472	US-08-964-268-4	Sequence 4, Appl
21	36	61.0	472	PCR-US95-08565-10	Sequence 10, Appl
22	34	57.6	558	US-08-836-567-6	Sequence 6, Appl
23	34	57.6	739	US-07-618-946B-22	Sequence 22, Appl
24	34	57.6	767	US-08-836-567-8	Sequence 8, Appl
25	34	57.6	814	US-07-618-946B-23	Sequence 23, Appl
26	33	55.9	50	US-08-377-687-13	Sequence 13, Appl
27	33	55.9	50	US-08-377-687-22	Sequence 22, Appl

28	33	55.9	50	2	US-08-777-192-13	Sequence 13, Appl
29	33	55.9	50	2	US-08-777-192-22	Sequence 22, Appl
30	33	55.9	50	4	US-08-971-982-13	Sequence 13, Appl
31	33	55.9	50	4	US-08-971-982-22	Sequence 22, Appl
32	33	55.9	327	4	US-09-290-640-66	Sequence 66, Appl
33	33	55.9	802	4	US-09-632-098-2	Sequence 2, Appl
34	33	55.9	902	1	US-08-396-479B-6	Sequence 6, Appl
35	33	55.9	902	1	US-08-818-823-6	Sequence 6, Appl
36	33	55.9	1219	4	US-08-882-046-5	Sequence 5, Appl
37	33	55.9	3567	2	US-07-642-734C-4	Sequence 4, Appl
38	33	55.9	3567	3	US-08-439-009A-4	Sequence 4, Appl
39	33	55.9	5588	4	US-09-036-987A-6	Sequence 6, Appl
40	33	55.9	5588	4	US-09-370-700-6	Sequence 6, Appl
41	32	54.2	49	1	US-08-304-051-1	Sequence 1, Appl
42	32	54.2	49	5	PCR-US95-11445-1	Sequence 1, Appl
43	32	54.2	113	1	US-07-668-648-10	Sequence 10, Appl
44	32	54.2	113	2	US-08-429-998-10	Sequence 10, Appl
45	32	54.2	113	2	US-08-431-333-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-07-728-215-30
; Sequence 30, Application US/07728215
; Patent No. 5962643
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pytela, Robert
; TITLE OF INVENTION: A No. 5962643el Integrin Beta Subunit and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07728,215
; FILING DATE: 19910711
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REFERENCE/DOCKET NUMBER: 31.815
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-728-215-30

Query Match 69.5%; Score 41; DB 2; Length 798;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RLRSGEPC 9
DB 122 RLRSGEPC 129

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RESULT 2
US-08-938-085A-30
; Sequence 30, Application US/08938085A
; Patent No. 6339148
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pytela, Robert
; TITLE OF INVENTION: A No. 6339148el Integrin Beta Subunit and Uses
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,085A
; FILING DATE: 26-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/738,215
; FILING DATE: 11-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 023070-080210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-938-085A-30

Query Match 69.5%; Score 41; DB 4; Length 798;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPO 9
Db 122 RLRSGEPO 129

RESULT 3
US-07-668-648-8
; Sequence 8, Application US/07668648
; Patent No. 5416192
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Plowman, Gregory D.
; TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,648
; FILING DATE: 19910819
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-668-648-8

Query Match 66.1%; Score 39; DB 1; Length 179;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPOC 10
Db 151 CRLKSGEWAC 160

RESULT 4
US-08-429-998-8
; Sequence 8, Application US/08429998
; Patent No. 5885961
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Plowman, Gregory D.
; TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,998
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/668,648
; FILING DATE: 13-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-429-998-8

Query Match 66.1%; Score 39; DB 2; Length 179;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEQC 10
Db 151 CRLKSGEWAC 160

RESULT 5
US-08-431-333-8
; Sequence 8, Application US/08431333
; Patent No. 5965723
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Plovman, Gregory D.
; TITLE OF INVENTION: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,333
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US 07/668,648
; FILING DATE: 13-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-431-333-8

Query Match 66.1%; Score 39; DB 2; Length 179;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEQC 10
Db 151 CRLKSGEWAC 160

RESULT 6
PCT-US91-02321-8
; Sequence 8, Application PC/TUS0102321
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Plovman, Gregory D.
; TITLE OF INVENTION: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02321
; FILING DATE: 19910403
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0071A-PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)728-4800
; TELEFAX: (206)448-4775
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02321-8

Query Match 66.1%; Score 39; DB 5; Length 179;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEQC 10
Db 151 CRLKSGEWAC 160

RESULT 7
US-08-867-676-3
; Sequence 3, Application US/08867676
; Patent No. 5866119
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW HUMAN RIBONUCLEASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,676
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
```

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0304 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1513102
US-08-867-676-3

Query Match 65.3%; Score 38.5; DB 2; Length 150;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSCE-PQC 10
DB 104 CRLTSGKYPQC 114

RESULT 8
US-08-867-676-1
Sequence 1, Application US/08867676
Patent No. 5866119
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW HUMAN RIBONUCLEASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: US/08/867,676
PRIOR APPLICATION NUMBER:
CLASSIFICATION: 435
APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0304 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SININOT01
CLONE: 2181484
US-08-867-676-1

Query Match 65.3%; Score 38.5; DB 2; Length 163;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSCE-PQC 10
DB 104 CRLTSGKYPQC 114

RESULT 9
US-08-560-098A-51
Sequence 51, Application US/08560098A
Patent No. 5976841
GENERAL INFORMATION:
APPLICANT: WNEBTD, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-560-098A-51

Query Match 64.4%; Score 38; DB 2; Length 477;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPQC 10
DB 326 QLKSGSPQC 334

RESULT 10
US-08-095-728B-6
Sequence 6, Application US/08095728B
Patent No. 5843642
GENERAL INFORMATION:
APPLICANT: DMITROVSKY, ETHAN
APPLICANT: WARRELL JR, RAYMOND P
APPLICANT: MILLER JR, WILSON H
APPLICANT: FRANKEL, STANLEY

```

; TITLE OF INVENTION: METHODS FOR THE DETECTION AND
; TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095,728B
; FILING DATE: 21-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/673,838
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38694-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-095-728B-6

Query Match 64.4% Score 38; DB 2; Length 560;
Best Local Similarity 77.8%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
Db 357 CRLRQEEPQ 365

RESULT 11
PCT-US92-02320A-6
; Sequence 6, Application PC/TUS9202320A
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute, For Cancer Research
; TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02320A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 675,084
; FILING DATE: 22-MAR-1991
; PRIOR APPLICATION DATA:

```

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; APPLICATION NUMBER: US 673,838
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38694-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 644-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-02320A-6

Query Match 64.4% Score 38; DB 5; Length 560;
Best Local Similarity 77.8%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
Db 357 CRLRQEEPQ 365

RESULT 12
US-08-095-728B-2
; Sequence 2, Application US/08095728B
; Patent No. 5843642
; GENERAL INFORMATION:
; APPLICANT: DMITROVSKY, ETHAN
; APPLICANT: WARRELL JR, RAYMOND P
; APPLICANT: MILLER JR, WILSON H
; APPLICANT: FRANKEL, STANLEY
; TITLE OF INVENTION: METHODS FOR THE DETECTION AND
; TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095,728B
; FILING DATE: 21-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/673,838
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38694-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-095-728B-2

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Query Match 64.4%; Score 38; DB 2; Length 797;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
Db 357 CRLRQEEPQ 365

RESULT 13
PCT-US92-02320A-2
; Sequence 2, Application PC/TUS9202320A
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute, For Cancer Research
; TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02320A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 675,084
; APPLICATION NUMBER: US 675,084
; FILING DATE: 22-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 673,838
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38694-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 644-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-02320A-2

Query Match 64.4%; Score 38; DB 5; Length 797;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
Db 357 CRLRQEEPQ 365

RESULT 14
US-08-972-008-4
; Sequence 4, Application US/08972008
; Patent No. 5942420
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: No. 5942420el Molecules of the Follistatin-Related
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/267,409
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/972,008
; FILING DATE: 1997-NOV-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-003DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214

; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,008
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-08-972-008-4

Query Match 62.7%; Score 37; DB 2; Length 71;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 10
Db 14 CRLMGRPRC 23

RESULT 15
US-09-267-409-4
; Sequence 4, Application US/09267409
; Patent No. 6410232
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: No. 6410232el Molecules of the Follistatin-Related
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/267,409
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/972,008
; FILING DATE: 1997-NOV-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-003DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-267-409-4

Query Match 62.7%; Score 37; DB 4; Length 71;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRLRSGEPOC 10
||: ||:|
Db 14 CRMLGGRPRC 23

Search completed: January 30, 2003, 13:33:42
Job time : 16 secs

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OM protein - protein search, using sw model

Run on: January 30, 2003, 13:33:26 ; Search time 10 seconds
(without alignments)
20.179 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLSGEPQC 10

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Searched: 122226 seqs, 20178551 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	41	69.5	543	10 US-09-778-927A-67	Sequence 67, Appl
2	41	69.5	662	10 US-09-778-927A-66	Sequence 66, Appl
3	41	69.5	798	9 US-10-072-841-30	Sequence 30, Appl
4	41	69.5	798	12 US-10-100-912-6	Sequence 6, Appl
5	37	62.7	263	9 US-10-101-392-2	Sequence 2, Appl
6	37	62.7	263	9 US-10-066-500-41	Sequence 41, Appl
7	37	62.7	263	9 US-10-053-107-4	Sequence 4, Appl
8	37	62.7	263	9 US-10-028-072-484	Sequence 484, Appl
9	37	62.7	798	9 US-10-117-295A-1	Sequence 1, Appl
10	36	61.0	458	9 US-09-843-905A-15	Sequence 15, Appl
11	35	59.3	1798	10 US-09-938-275-9	Sequence 9, Appl
12	35	59.3	1798	10 US-09-845-583-8	Sequence 8, Appl
13	35	59.3	1799	10 US-09-845-583-6	Sequence 6, Appl
14	35	59.3	1801	10 US-09-938-275-8	Sequence 8, Appl
15	35	59.3	3635	10 US-09-845-583-2	Sequence 2, Appl
16	34	57.6	757	10 US-09-919-603-3	Sequence 3, Appl
17	33	55.9	50	10 US-09-759-584-13	Sequence 13, Appl
18	33	55.9	50	10 US-09-759-584-22	Sequence 22, Appl
19	33	55.9	204	10 US-09-948-018-18	Sequence 18, Appl

20	33	55.9	206	10 US-09-887-855-5	Sequence 5, Appl
21	33	55.9	268	10 US-09-815-242-11977	Sequence 11977, A
22	33	55.9	270	10 US-09-764-855-145	Sequence 145, App
23	33	55.9	327	10 US-09-802-669-66	Sequence 66, Appl
24	33	55.9	334	9 US-09-738-626-5849	Sequence 5849, App
25	33	55.9	372	9 US-10-028-072-106	Sequence 106, App
26	33	55.9	374	10 US-09-887-855-2	Sequence 2, Appl
27	32.5	55.1	273	10 US-09-764-864-1421	Sequence 1421, App
28	32.5	55.1	316	10 US-09-764-864-1036	Sequence 1036, App
29	32	54.2	44	10 US-09-925-299-1094	Sequence 1094, App
30	32	54.2	54	10 US-09-925-299-1361	Sequence 1361, App
31	32	54.2	61	10 US-09-925-299-1513	Sequence 1513, App
32	32	54.2	62	10 US-09-925-301-1475	Sequence 1475, App
33	32	54.2	68	10 US-09-764-855-95	Sequence 95, Appl
34	32	54.2	76	10 US-09-764-870-347	Sequence 347, App
35	32	54.2	76	10 US-09-764-853-548	Sequence 548, App
36	32	54.2	78	10 US-09-925-299-1091	Sequence 1091, App
37	32	54.2	80	10 US-09-925-301-1476	Sequence 1476, App
38	32	54.2	84	10 US-09-925-299-1518	Sequence 1518, App
39	32	54.2	89	10 US-09-925-297-646	Sequence 646, App
40	32	54.2	103	10 US-09-925-302-830	Sequence 830, App
41	32	54.2	104	10 US-09-764-855-111	Sequence 111, App
42	32	54.2	105	10 US-09-864-761-37162	Sequence 37162, A
43	32	54.2	113	10 US-09-925-301-1672	Sequence 1672, App
44	32	54.2	116	10 US-09-764-877-1993	Sequence 1993, App
45	32	54.2	119	10 US-09-925-297-867	Sequence 867, App

ALIGNMENTS

RESULT 1

US-09-778-927A-67

; Sequence 67, Application US/09778927A
; Patent No. US20020068342A1

; GENERAL INFORMATION:

; APPLICANT: KHOSRAVI, Rami et al.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL

; FILE REFERENCE: 2786-0160P

; CURRENT APPLICATION NUMBER: US/09/778,927A

; PRIOR FILING DATE: 2001-02-08

; PRIOR APPLICATION NUMBER: IL134453

; PRIOR FILING DATE: 2000-02-09

; PRIOR APPLICATION NUMBER: IL135341

; NUMBER OF SEQ ID NOS: 81

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 67

; LENGTH: 543

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (1)-(543)

; OTHER INFORMATION: Xaa - any amino acid, unknown, or other

US-09-778-927A-67

Query Match 69.5%; Score 41; DB 10; Length 543;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPC 9

Db 122 RLRSGEPC 129

|||||||

RESULT 2

US-09-778-927A-66

; Sequence 66, Application US/09778927A

; Patent No. US20020068342A1

; GENERAL INFORMATION:

; APPLICANT: KHOSRAVI, Rami et al.

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; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778, 927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 66
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(662)
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-66

Query Match          69.5%; Score 41; DB 10; Length 662;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLRSGEPQ 9
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Db      122 RLRSGEPQ 129

RESULT 3
US-10-072-841-30
; Sequence 30, Application US/10072841
; Patent No. US20020164708A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; Pytela, Robert
; TITLE OF INVENTION: A NO. US20020164708A1e1 Integrin Beta Subunit and Uses
; Theroef
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/072,841
; FILING DATE: 06-Feb-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,215
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8717
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-072-841-30

Query Match          69.5%; Score 41; DB 9; Length 798;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLRSGEPQ 9
      |||||
Db      122 RLRSGEPQ 129

RESULT 4
US-10-100-912-6
; Sequence 6, Application US/10100912
; Patent No. US20020137459A1
; GENERAL INFORMATION:
; APPLICANT: Geller, Herbert M.
; APPLICANT: Meiners, Sally
; TITLE OF INVENTION: Neurite Outgrowth and Guidance by Tenascin-C
; FILE REFERENCE: 601-1-094
; CURRENT APPLICATION NUMBER: US/10/100,912
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: PCT/US00/11647
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/132,137
; PRIOR FILING DATE: 1999-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-100-912-6

Query Match          69.5%; Score 41; DB 12; Length 798;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLRSGEPQ 9
      |||||
Db      122 RLRSGEPQ 129

RESULT 5
US-10-101-392-2
; Sequence 2, Application US/10101392
; Patent No. US20020164714A1
; GENERAL INFORMATION:
; APPLICANT: Duan, et al.
; TITLE OF INVENTION: Follistatin-3
; FILE REFERENCE: PF388
; CURRENT APPLICATION NUMBER: US/10/101,392
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/141,027
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/656,248
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-392-2

Query Match          62.7%; Score 37; DB 9; Length 263;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRLRSGEPC 10
      ||: | |
Db      110 CRLGGPRPC 119
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RESULT 6
US-10-066-500-41
; Sequence 41, Application US/10066500
; Patent No. US20020177165A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C7
; CURRENT APPLICATION NUMBER: US/10/066,500
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066840
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 60/069694
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/095998
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/097000
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/099601
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100858
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/109304
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/139695
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/145070
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/149396
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 08/918874
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 08/933821
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 08/960507
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 09/114844
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: 09/136801
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 09/136804
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 09/136828
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 09/158342
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/202088
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: 09/254311
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: 09/254460
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/254465
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: 09/284663
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 09/332928
; PRIOR FILING DATE: 1999-06-14
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; PRIOR FILING DATE: 1999-06-14
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; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 09/333077
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/403296

;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/403297
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/423741
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: 09/423844
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 09/522342
;; PRIOR FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: 09/548815
;; PRIOR FILING DATE: 2000-04-13
;; PRIOR APPLICATION NUMBER: 09/664610
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 09/665350
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 09/709238
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 09/767609
;; PRIOR FILING DATE: 2001-01-22
;; PRIOR APPLICATION NUMBER: 09/802706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 09/808689
;; PRIOR FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 09/866028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 09/870574
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: 09/872035
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: 09/886342
;; PRIOR FILING DATE: 2001-06-19
;; PRIOR APPLICATION NUMBER: PCT/US98/14552
;; PRIOR FILING DATE: 1998-07-14
;; PRIOR APPLICATION NUMBER: PCT/US98/18824
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/US98/19093
;; PRIOR FILING DATE: 1998-09-14
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: 1998-09-16
;; PRIOR APPLICATION NUMBER: PCT/US98/19437
;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: PCT/US98/24855
;; PRIOR FILING DATE: 1998-11-20
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: 1998-12-01
;; PRIOR APPLICATION NUMBER: PCT/US98/25190
;; PRIOR FILING DATE: 1998-11-25
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: PCT/US99/20111
;; PRIOR FILING DATE: 1999-09-01
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 62.7%; Score 37; DB 9; Length 263;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

OY 1 CRLRSGEPOC 10
DB 110 CRLMGRPRC 119

RESULT 7
US-10-053-107-4
; Sequence 4, Application US/10053107
; Publication No. US20020192752A1
; GENERAL INFORMATION:

;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
;; FILE REFERENCE: P3033R1C1
;; CURRENT APPLICATION NUMBER: US/10/053,107
;; CURRENT FILING DATE: 2002-01-17
;; PRIOR APPLICATION NUMBER: 60/099601
;; PRIOR FILING DATE: 1999-09-09
;; PRIOR APPLICATION NUMBER: 60/107783
;; PRIOR FILING DATE: 1998-11-10
;; PRIOR APPLICATION NUMBER: 60/108802
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/113296
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/131291
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/151733
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/209832
;; PRIOR FILING DATE: 2000-06-05
;; PRIOR APPLICATION NUMBER: 60/232887
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 09/218517
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: PCT/US99/00106
;; PRIOR FILING DATE: 1999-01-05
;; PRIOR APPLICATION NUMBER: PCT/US99/20111
;; PRIOR FILING DATE: 1999-09-01
;; PRIOR APPLICATION NUMBER: PCT/US00/04342
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/05601
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: PCT/US00/13705
;; PRIOR FILING DATE: 2000-05-17
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: PCT/US00/14941
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;; PRIOR FILING DATE: 2000-08-23
;; PRIOR APPLICATION NUMBER: PCT/US00/23328
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; PRIOR APPLICATION NUMBER: PCT/US01/17800
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 14
;; SEQ ID NO 4
;; LENGTH: 263
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-053-107-4

Query Match 62.7%; Score 37; DB 9; Length 263;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

OY 1 CRLRSGEPOC 10
DB 110 CRLMGRPRC 119

Db 110 CRLGGRPC 119

RESULT 8

US-10-028-072-484
Sequence 484, Application US/10028072
Publication No. US20030004311A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063561
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704
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PRIOR FILING DATE: 1997-11-07
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PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600

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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084637
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; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086414
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086430
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 19/98-06-11
; PRIOR APPLICATION NUMBER: 60/089522
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match      62.7%; Score 37; DB 9; Length 263;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLRSRGPQC 10
Db 110 CRMLGRRPC 119

RESULT 9
US-10-117-295A-1
; Sequence 1, Application US/10117295A
; Publication No. US20020182678A1

; GENERAL INFORMATION:
; APPLICANT: GARRIDO PAVON, Juan Jose
; APPLICANT: LLANES RUIZ, Diego
; APPLICANT: BABANCHO MEDINA, Manuel
; APPLICANT: JIMENEZ MARIN, Angeles Maria
; TITLE OF INVENTION: CD29 PIG PROTEIN, NUCLEIC ACID CODING FOR SAID PROTEIN
; FILE REFERENCE: 9256-13US
; CURRENT APPLICATION NUMBER: US/10/117,295A
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: PCT/ES00/00374
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: P9902193
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 1
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Pig
US-10-117-295A-1

Query Match      62.7%; Score 37; DB 9; Length 798;
Best Local Similarity 87.5%; Pred. No. 76;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSRGPQC 9
Db 122 QLRSRGPQC 129

RESULT 10
US-09-843-905A-15
; Sequence 15, Application US/09843905A
; Patent No. US20020186683A1
; GENERAL INFORMATION:
; APPLICANT: Bird, Timothy A.
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES
; FILE REFERENCE: 2990-A
; CURRENT APPLICATION NUMBER: US/09/843,905A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,198
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-843-905A-15

Query Match      61.0%; Score 36; DB 9; Length 458;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RLRSRGPQC 10
Db 302 RLRSRGPQC 310

RESULT 11
US-09-938-275-9
; Sequence 9, Application US/09938275
; Patent No. US2002011309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: Of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P55268
; DATABASE ENTRY DATE: 1996-10-01
US-09-938-275-9

Query Match      59.3%; Score 35; DB 10; Length 1798;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQPC 10
Db 1428 CRDEGQPC 1437

RESULT 12
US-09-845-583-8
; Sequence 8, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-583-8

Query Match      59.3%; Score 35; DB 10; Length 1798;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQPC 10
Db 1428 CRDEGQPC 1437

RESULT 13
US-09-845-583-6
; Sequence 6, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-845-583-6

Query Match      59.3%; Score 35; DB 10; Length 1799;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQPC 10
Db 1429 CRDEGQPC 1438

RESULT 14
US-09-938-275-8
; Sequence 8, Application US/09938275
; Patent No. US2002011309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1801
; TYPE: PRT
; ORGANISM: Rattus No. US2002011309A1vegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P15800
; DATABASE ENTRY DATE: 1990-04-01
US-09-938-275-8

Query Match      59.3%; Score 35; DB 10; Length 1801;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQPC 10
Db 1431 CRDEGQPC 1440

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US-09-845-583-2
; Sequence 2, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3635
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583-2

Query Match      59.3%; Score 35; DB 10; Length 3635;
Best Local Similarity 60.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQPC 10
Db 1847 CVLRNGRTQC 1856

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Search completed: January 30, 2003, 13:37:27
Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 30, 2003, 13:32:01 ; Search time 15 seconds
(without alignments)
64.090 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLRSGEPQC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	45	76.3	3051	2 S42373	hypothetical prote
2	41	69.5	798	2 B27079	fibronectin recept
3	40	67.8	892	2 T15195	hypothetical prote
4	38.5	65.3	150	2 S72361	pancreatic ribonuc
5	38	64.4	394	2 JS0600	t-plasminogen acti
6	38	64.4	431	2 JS0599	t-plasminogen acti
7	38	64.4	477	1 A34369	t-plasminogen acti
8	38	64.4	477	2 JS0598	t-plasminogen acti
9	38	64.4	560	2 A60198	PML-1 protein - hu
10	38	64.4	589	2 S42517	PML protein, splic
11	38	64.4	589	2 S44381	PML protein, splic
12	38	64.4	593	2 B40045	probable transcrip
13	38	64.4	633	2 S19244	gene Myl protein -
14	38	64.4	634	2 AG0252	probable DEAD box
15	38	64.4	636	2 E90943	probable enzyme [i
16	38	64.4	636	2 A85792	probable enzyme 22
17	38	64.4	636	2 AF0725	probable ATP-depen
18	38	64.4	636	2 H64941	probable ATP-depen
19	38	64.4	641	2 A40045	probable transcrip
20	38	64.4	646	2 E82133	ATP-dependent heli
21	38	64.4	798	2 S01659	integrin beta-1 ch
22	38	64.4	799	1 LUNSF8	fibronectin recept
23	38	64.4	799	2 JC4126	integrin beta olig
24	38	64.4	802	2 S42518	PML protein, splic
25	38	64.4	802	2 S44382	PML protein, splic
26	38	64.4	860	2 S42516	PML protein, splic
27	38	64.4	860	2 S44380	PML protein, splic
28	38	64.4	955	4 C40045	probable transcrip
29	38	64.4	955	4 C40045	probable transcrip

30	37	62.7	64	2 T16954	hypothetical prote
31	37	62.7	161	2 E71078	hypothetical prote
32	37	62.7	393	2 T16046	hypothetical prote
33	37	62.7	484	2 T25731	hypothetical prote
34	37	62.7	773	2 I46059	beta-1 integrin su
35	36	61.0	151	2 E69077	hypothetical prote
36	36	61.0	354	2 T22274	hypothetical prote
37	36	61.0	405	2 A82130	transcription regu
38	36	61.0	472	1 WZECDD	deoxyribodipyrimid
39	36	61.0	472	2 E90720	deoxyribodipyrimid
40	36	61.0	472	2 C85571	hypothetical prote
41	36	61.0	564	1 VHXPMV	major structural n
42	36	61.0	798	2 A28193	integrin beta-1 ch
43	36	61.0	798	2 B28193	integrin beta-1 c
44	36	61.0	2767	1 UIHU	thyroglobulin prec
45	35	59.3	121	2 JX0279	ribonuclease CL2 -

ALIGNMENTS

RESULT 1

S42373
hypothetical protein T20G5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: S42373
R;Smith, A.
submitted to the EMBL Data Library, March 1994
A;Reference number: S42368
A;Accession: S42373
A;Molecule type: DNA
A;Residues: 1-3051 <SMI>
A;Cross-references: EMBL:Z30423; NID:g458479; PID:g458485
C;Genetics:
A;Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146
C;Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronectin
F;512-679/Domain: von Willebrand factor type A repeat homology <VWAL>
F;754-793/Domain: fibronectin type II repeat homology <2F1>
F;1201-1244/Domain: EGF homology <EGF>

Query Match 76.3%; Score 45; DB 2; Length 3051;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQC 10

Db 1372 CRLMGEPKC 1381

RESULT 2

B27079
fibronectin receptor beta chain precursor - human
N;Alternate names: CD29 antigen; integrin beta-1 chain
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999
C;Accession: B27079
R;Argaves, W.S.; Suzuki, S.; Arai, H.; Thompson, K.; Pierschbacher, M.D.; Ruoslahti, J.
J. Cell Biol. 105, 1183-1190, 1987
A;Title: Amino acid sequence of the human fibronectin receptor.
A;Reference number: A27079; MUID:88007843; PMID:2958481
A;Accession: B27079
A;Molecule type: mRNA
A;Residues: 1-798 <ARG>
A;Cross-references: EMBL:X07979; NID:g31441; PIDN:CAA30790.1; PID:g31442
C;Genetics:
A;Gene: GDB:ITGB1; FNRB
A;Cross-references: GDB:118732; OMIM:135630
A;Map position: 10p11.2-10p11.2
C;Superfamily: integrin beta chain; laminin-type EGF-like homology
C;Keywords: alternative splicing; duplication; heterodimer; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-798/Product: fibronectin receptor beta chain #status predicted <MAT>

Query Match 69.5%; Score 41; DB 2; Length 798;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPO 9
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 Db 122 RLRSGEPO 129

RESULT 3
 T15195
 Hypothetical protein F55A12.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T15195
 R:Pauley, A.; Gattung, S.
 Submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid F55A12.
 A:Reference number: Z18305
 A:Accession: T15195
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-892 <PAU>
 A:Cross-references: EMBL:AF003130; NID:g2088663; PID:g2088671; PIDN:AAB54129.1; GSPDB:GN
 A:Experimental source: strain Bristol N2; clone F55A12
 C:Genetics:
 A:Gene: CESP:F55A12.1
 A:Map position: 1
 A:Introns: 55/3; 75/3; 216/2; 460/3; 517/3; 558/1; 673/3; 753/3; 856/2

Query Match 67.8%; Score 40; DB 2; Length 892;
 Best Local Similarity 60.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPO 10
 |||||
 Db 511 CRFSGDPPC 520

RESULT 4
 S72361
 pancreatic ribonuclease (EC 3.1.27.5) k6 precursor - human
 N:Alternate names: RNase k6
 C:Species: Homo sapiens (man)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 08-May-1998
 C:Accession: S72361; S72362
 R:Rosenberg, H.F.; Dyer, K.D.
 Submitted to the EMBL Data Library, July 1996
 A:Description: Molecular cloning and characterization of a novel human ribonuclease (RNA
 A:Reference number: S72361
 A:Accession: S72361
 A:Molecule type: DNA
 A:Residues: 1-150 <NOS>
 A:Cross-references: EMBL:U64998; NID:g1513101; PID:g1513102
 R:Rosenberg, H.F.; Dyer, K.D.
 Nucleic Acids Res. 24, 3507-3513, 1996
 A:Title: Molecular cloning and characterization of a novel human ribonuclease (RNase k6)
 A:Reference number: S72362; MUID:96433147; PMID:8836175
 A:Accession: S72362
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 24-150 <ROW>
 A:Cross-references: EMBL:U64998
 C:Genetics:
 A:Map position: 14
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid degradation
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-150/Product: pancreatic ribonuclease #status predicted <MAT>
 F:46-104/60-114/78-129; 85-92/Disulfide bonds: #status predicted
 F:55,100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.3%; Score 38.5; DB 2; Length 150;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSGE-POC 10
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 Db 104 CRLTSGKYPQC 114

RESULT 5
 JS0600
 t-plasminogen activator (EC 3.4.21.68) gamma precursor - common vampire bat
 N:Alternate names: tissue plasminogen activator
 C:Species: Desmodus rotundus (common vampire bat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C:Accession: JS0600
 R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.;
 Gene 105, 229-237, 1991
 A:Title: The plasminogen activator family from the salivary gland of the vampire bat
 A:Reference number: JS0597; MUID:92039036; PMID:1937019
 A:Accession: JS0600
 A:Molecule type: mRNA
 A:Residues: 1-394 <KRA>
 A:Cross-references: GB:M63990; NID:g166078; PIDN:AAA31595.1; PID:g166079
 A:Note: The authors translated the codon ATC for residue 75 as Thr
 C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-36/Domain: propeptide #status predicted <PRO>
 F:37-394/Product: plasminogen activator gamma #status predicted <PLA>
 F:45-126/Domain: kringle homology <KRG>
 F:143-388/Domain: trypsin homology <TRY>
 F:45-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bond
 F:142-143/Cleavage site: His-Ser (plasma) #status predicted
 F:189,238,345/Active site: His, Asp, Ser #status predicted
 F:315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.4%; Score 38; DB 2; Length 394;
 Best Local Similarity 66.7%; Pred. No. 34;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPOC 10
 |||||
 Db 243 QLKSGSPQC 251

RESULT 6
 JS0599
 t-plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat
 N:Alternate names: tissue plasminogen activator
 C:Species: Desmodus rotundus (common vampire bat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C:Accession: JS0599
 R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.;
 Gene 105, 229-237, 1991
 A:Title: The plasminogen activator family from the salivary gland of the vampire bat
 A:Reference number: JS0597; MUID:92039036; PMID:1937019
 A:Accession: JS0599
 A:Molecule type: mRNA
 A:Residues: 1-431 <KRA>
 A:Cross-references: GB:M63989; NID:g166076; PIDN:AAA31594.1; PID:g166077
 C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-36/Domain: propeptide #status predicted <PRO>
 F:37-431/Product: plasminogen activator beta #status predicted <PLA>
 F:41-74/Domain: EGF homology <EGF>
 F:82-163/Domain: kringle homology <KRG>
 F:180-425/Domain: trypsin homology <TRY>
 F:41-52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide
 F:139,352/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:179-180/Cleavage site: His-Ser (plasma) #status predicted
 F:226,275,382/Active site: His, Asp, Ser #status predicted

F:345-361,378-406/Disulfide bonds: #status predicted

Query Match 64.4%; Score 38; DB 2; Length 431;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPOC 10
:||| |||

Db 280 QLKSGSPQC 288

RESULT 7

A34369
t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)
C:Species: Megaderma lyra
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Gardell, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Jacob
J. Biol. Chem. 264, 17947-17952, 1989
A:Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plasmin
A:Reference number: A34369; MUID:90036867; PMID:2509450
A:Accession: A34369
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-477 <GAR>
A:Cross-references: GB:J05082; NID:gl66080; PIDN:AAA31596.1; PID:gl66081
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:37-47/Domain: propeptide #status predicted <PRO>
F:42-79/Domain: plasminogen activator #status predicted <PLA>
F:87-120/Domain: fibronectin type I repeat homology <IFA>
F:128-209/Domain: kringle homology <KRG>
F:226-471/Domain: trypsin homology <TRY>
F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
F:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 64.4%; Score 38; DB 1; Length 477;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPOC 10
:||| |||

Db 326 QLKSGSPQC 334

RESULT 8

JS0598
t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor - common vampire bat
N:Alternate names: tissue plasminogen activator
C:Species: Desmodus rotundus (common vampire bat)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: JS0598
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don
Gene 105, 229-237, 1991
A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A:Reference number: JS0598; MUID:92039036; PMID:1937019
A:Accession: JS0598
A:Molecule type: mRNA
A:Residues: 1-477 <KRA>
A:Cross-references: GB:M63988; NID:gl66074; PIDN:AAA31593.1; PID:gl66075
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-36/Domain: propeptide #status predicted <PRO>
F:37-47/Domain: plasminogen activator alpha-2 #status predicted <PLA>
F:42-79/Domain: fibronectin type I repeat homology <IFA>
F:87-120/Domain: EGF homology <EGF>
F:128-209/Domain: kringle homology <KRG>
F:226-471/Domain: trypsin homology <TRY>
F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
F:185,398/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:225-226/Cleavage site: His-Ser (plasmin) #status predicted
F:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 64.4%; Score 38; DB 2; Length 477;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPOC 10
:||| |||

Db 326 QLKSGSPQC 334

RESULT 9

A40044
PML-1 protein - human
N:Alternate names: promyelocytic leukemia protein
C:Species: Homo sapiens (man)
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 02-Aug-2002
C:Accession: A40044
R:Kakizuka, A.; Miller Jr., W.H.; Umesono, K.; Warrell Jr., R.P.; Frankel, S.R.; Murt
Cell 66, 663-674, 1991
A:Title: Chromosomal translocation t(15;17) in human acute promyelocytic leukemia fus
A:Reference number: A40044; MUID:91347368; PMID:1652368
A:Accession: A40044
A:Molecule type: mRNA
A:Residues: 1-560 <KAK>
A:Cross-references: GB:M73778; NID:gl90114; PIDN:AAA60125.1; PID:gl90115
C:Genetics:
A:Gene: GDB:PML; MYL
A:Cross-references: GDB:127542; OMIM:102578
A:Map position: 15q22-15q22
C:Superfamily: human PML-1 protein; RING finger homology
C:Keywords: DNA binding; transcription regulation; zinc
F:53-97/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 560;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
||||| |||

Db 357 CRLRQEPQ 365

RESULT 10

A60198
Myl protein - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 02-Aug-2002
C:Accession: A60198
R:Pandolfi, P.P.; Grignani, F.; Alcalay, M.; Mencarelli, A.; Biondi, A.; Lococo, F.;
Oncogene 6, 1285-1292, 1991
A:Title: Structure and origin of the acute promyelocytic leukemia myl/RARalpha cDNA a
A:Reference number: A60198; MUID:91319412; PMID:1650447
A:Accession: A60198
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-589 <PAN>
A:Note: the authors' translation is shown for residues 543-549; the corresponding nuc
C:Superfamily: human PML-1 protein; RING finger homology
C:Keywords: zinc
F:31-75/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 589;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
||||| |||

Db 335 CRLRQEPQ 343

RESULT 11

A.;Title: The PML-RARalpha fusion mRNA generated by the t(15;17) translocation in acute promyelocytic leukemia

A.;Reference number: A40045; MUID:91347369; PMID:1652369

A.;Accession: B40045

A.;Status: preliminary

A.;Molecule type: mRNA

A.;Residues: 1-593 <DE2>

C.;Superfamily: human PML-1 protein; RING finger homology

C.;Keywords: zinc

F;53-97/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 593;

Best Local Similarity 77.8%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9

DB 357 CRLRQEEPPQ 365

||||| ||||

RESULT 14

S19244

gene Myl protein - human

C.;Species: Homo sapiens (man)

C.;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 02-Aug-2002

C.;Accession: S19244

R.;Kastner, P.; Perez, A.; Lutz, Y.; Rochette-Egly, C.; Gaub, M.P.; Durand, B.; Lanotti, E.M.B. J. 11, 629-642, 1992

A.;Title: Structure, localization and transcriptional properties of two classes of retinoid X receptor-related proteins

A.;Reference number: S19244; MUID:92164652; PMID:1311253

A.;Accession: S19244

A.;Status: preliminary

A.;Molecule type: mRNA

A.;Residues: 1-633 <RAS>

A.;Cross-references: EMBL:Y63131; NID:g34813; PIDN:CAA44841.1; PID:g34814

C.;Superfamily: human PML-1 protein; RING finger homology

C.;Keywords: DNA binding; transcription regulation; zinc

F;53-97/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 633;

Best Local Similarity 77.8%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9

DB 357 CRLRQEEPPQ 365

||||| ||||

RESULT 15

AG0252

probable DEAD box family helicase YPO2071 [imported] - Yersinia pestis (strain CO92)

C.;Species: Yersinia pestis

C.;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C.;Accession: AG0252

R.;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.; Deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, N. Nature 413, 523-527, 2001

A.;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A.;Reference number: AB0001; MUID:21470413; PMID:11586360

A.;Accession: AG0252

A.;Status: preliminary

A.;Molecule type: DNA

A.;Residues: 1-634 <KUR>

A.;Cross-references: GB:AL590842; PIDN:CAC90883.1; PID:g15980082; GSPDB:GN00175

C.;Genetics:

A.;Gene: YPO2071

Query Match 64.4%; Score 38; DB 2; Length 634;

Best Local Similarity 75.0%; Pred. No. 52;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRLRSGEP 8

Db 557 CRLRGDP 564
||||| |:

Search completed: January 30, 2003, 13:33:21
Job time : 16 secs

20030130 134038

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 30, 2003, 13:31:56 ; Search time 11 seconds
(without alignments)
37.706 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLRSGEPQC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	45	76.3	3767	MUA3_CAEEL	P34576 caenorhabdi
2	41	69.5	798	ITB1_HUMAN	P05556 homo sapien
3	38.5	65.3	150	RNK6_AOTTR	O46528 aotus trivi
4	38.5	65.3	150	RNK6_CERAE	O46534 cercopithec
5	38.5	65.3	150	RNK6_GORGO	O46532 gorilla gor
6	38.5	65.3	150	RNK6_HUMAN	Q93091 homo sapien
7	38.5	65.3	150	RNK6_MACMU	O46533 macaca mula
8	38.5	65.3	150	RNK6_MIOTA	O46531 miopithecus
9	38.5	65.3	150	RNK6_PANTR	O46525 pan troglod
10	38.5	65.3	150	RNK6_PAPHA	O46527 papio hamad
11	38.5	65.3	150	RNK6_SAGOE	O46530 saguinus oe
12	38	64.4	394	URTB_DESRO	P49150 desmodus ro
13	38	64.4	431	URTB_DESRO	P98121 desmodus ro
14	38	64.4	477	URTB_DESRO	P15638 desmodus ro
15	38	64.4	636	YOAA_ECOLI	P76257 escherichia
16	38	64.4	798	ITB1_MOUSE	P09055 mus musculus
17	38	64.4	799	ITB1_RAT	P49134 rattus norv
18	38	64.4	882	ITB1_HUMAN	P53712 bos taurus
19	37.5	63.6	150	RNK6_SAIISC	P53713 felis silve
20	37	62.7	64	YSXB_CAEEL	O46526 pongo pygma
21	37	62.7	393	YSH8_CAEEL	P00914 escherichia
22	37	62.7	719	DEND_RAT	P26578 machupo vir
23	37	62.7	773	ITB1_BOVIN	P12607 xenopus lae
24	37	62.7	798	ITB1_FELCA	P12606 xenopus lae
25	36.5	61.9	150	RNK6_PONPY	P01266 homo sapien
26	36	61.0	472	PHR_ECOLI	P81476 gallus gall
27	36	61.0	564	NCAP_MACHU	P34026 xanthomonas
28	36	61.0	798	ITB0_XENLA	Q9qzy6 cavia porce
29	36	61.0	798	ITB1_XENLA	
30	36	61.0	2768	1 THYG_HUMAN	
31	35	59.3	121	RNL2_CHICK	
32	35	59.3	283	1 GSPK_XANCP	
33	35	59.3	332	1 CLC3_CAVPO	

34	35	59.3	591	1 GRN_CAVPO	P28797 cavia porce
35	35	59.3	888	1 KLTW_MOUSE	P08923 mus musculus
36	35	59.3	1115	1 GPCR_LINMT	P46023 lymanaea sta
37	35	59.3	1798	1 LMB2_HUMAN	P55268 homo sapien
38	35	59.3	1799	1 LMB2_MOUSE	O61292 mus musculus
39	35	59.3	1801	1 LMB2_RAT	P15800 rattus norv
40	35	59.3	3718	1 LMA5_MOUSE	O61001 mus musculus
41	34	57.6	146	1 ANGI_MACMU	O84963 macaca mula
42	34	57.6	252	1 VPHE_NPVAC	P24728 autographa
43	34	57.6	640	1 YOAA_HAEIN	P44680 haemophilus
44	34	57.6	757	1 COMP_HUMAN	P49747 homo sapien
45	34	57.6	788	1 UGS3_SOLITU	Q43847 solanum tub

ALIGNMENTS

RESULT 1
MUA3_CAEEL
ID MUA3_CAEEL STANDARD; PRT; 3767 AA.
AC P34576; Q9UAI3; Q21340;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane cell adhesion receptor mua-3 precursor.
GN MUA-3 OR K08E5.3/720G5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Caenorhabditis.
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Lu Z., Vogel B., Hedgecock E.;
RT "mua-3 mRNA splicing pattern revealed";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Berks M., Smith A., Kershaw J.K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: Involved in cell adhesion.
CC - SIMILARITY: CONTAINS 52 EGF-LIKE DOMAINS.
CC - SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
CC - SIMILARITY: CONTAINS 2 SEA DOMAINS.
CC - SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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DR EMBL; AF139060; AAD29428.1; -
DR EMBL; Z30974; CAA83226.2; -
DR EMBL; Z30423; CAA83226.2; JOINED.
DR EMBL; Z30423; CAC42345.1; -
DR EMBL; Z30974; CAC42345.1; JOINED.
DR PIR; S42373; S42373.
DR HSSP; P17301; IAOX.
DR WormPep; K08E5.3; CE28049.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF-Ca.
DR InterPro; IPR002172; LDL_recept_A.
DR InterPro; IPR000082; SEA_domain.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF000008; EGF; 33.
DR Pfam; PF000057; ldl_recept_a; 3.
DR Pfam; PF01390; SEA; 2.

Query Match 76.3%; Score 45; DB 1; Length 3767;
 Best Local Similarity 70.0%; Pred. No. 4.2;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSRGPQC 10
 III IIII
 Db 2088 CRLMGGEPC 2097

RESULT 2

ITB1_HUMAN STANDARD; PRT: 798 AA.
 ID ITB1_HUMAN STANDARD; PRT: 798 AA.
 AC P05556; P78466; Q13089; Q14647; Q13090; Q13212; Q13091;
 AC Q14622;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Integrin beta-1 precursor (Fibronectin receptor beta subunit)
 DE (CD29 antigen) (Integrin VLA-4 beta subunit).
 GN ITGB1 OR FNBR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BETA-1A).
 RC TISSUE=Placenta;
 RX MEDLINE=88007843; PubMed=2958481;
 RA Agraves W.S., Suzuki S., Arai H., Thompson K., Pierschbacher M.D.,
 RA Ruoslahti E.;
 RT "Amino acid sequence of the human fibronectin receptor.";
 RL J. Cell Biol. 105:1183-1190(1987).
 RN [2]
 RP SEQUENCE OF 717-757 FROM N.A., AND CHARACTERIZATION OF BETA-1B.
 RX MEDLINE=93209984; PubMed=7681433;
 RA Balzac F., Belkin A.M., Koteliarsky V.E., Balabanov Y.V., Altruda F.,
 RA Silengo L., Tarone G.;
 RT "Expression and functional analysis of a cytoplasmic domain variant of
 the beta 1 integrin subunit.";
 RL J. Cell Biol. 121:171-178(1993).
 RN [3]
 RP SEQUENCE OF 717-757 FROM N.A., AND FUNCTION.
 RX MEDLINE=95014744; PubMed=7523423;
 RA Balzac F., Retta S.F., Albini A., Melchiorri A., Koteliarsky V.E.,
 RA Geuna M., Silengo L., Tarone G.;
 RT "Expression of beta 1B integrin isoform in CHO cells results in a
 dominant negative effect on cell adhesion and motility.";
 RL J. Cell Biol. 127:557-565(1994).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BETA-1A; BETA-1B; BETA-1C AND
 BETA-1D).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=95398646; PubMed=7545396;
 RA Zhidkova N.I., Belkin A.M., Mayne R.;
 RT "Novel isoform of beta 1 integrin expressed in skeletal and cardiac
 muscle.";
 RL Biochem. Biophys. Res. Commun. 214:279-285(1995).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1B).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=91065539; PubMed=2249781;
 RA Altruda F., Cervella P., Tarone G., Botta C., Balzac F., Stefanuto G.,
 RA Silengo L.;
 RT "A human integrin beta 1 subunit with a unique cytoplasmic domain
 generated by alternative mRNA processing.";
 RL Gene 95:261-266(1990).
 RN [6]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1D).
 RX MEDLINE=95377431; PubMed=7544298;
 RA van der Flier A., Kuikman I., Baudoin C., van der Neut R.,
 RA Sonnenberg A.;
 RT "A novel beta 1 integrin isoform produced by alternative splicing;

RT unique expression in cardiac and skeletal muscle.";
 RL REBS Lett. 369:340-344(1995).
 RN [7]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BETA-1A AND BETA-1C).
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=92202279; PubMed=1551917;
 RA Languino L.R., Ruoslahti E.;
 RT "An alternative form of the integrin beta 1 subunit with a variant
 cytoplasmic domain.";
 RL J. Biol. Chem. 267:7116-7120(1992).
 RN [8]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1C-2).
 RX MEDLINE=98161905; PubMed=9494094;
 RA Svineng G., Faessler R., Johansson S.;
 RT "Identification of beta1c-2, a novel variant of the integrin beta1
 subunit generated by utilization of an alternative splice acceptor
 site in exon C.";
 RL Biochem. J. 330:1255-1263(1998).
 CC -1- FUNCTION: INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-10/BETA-1
 1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-
 1/BETA-1 AND ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED
 SEQUENCE G-F-P-G-E-R IN COLLAGEN. INTEGRINS ALPHA-2/BETA-1, ALPHA-
 3/BETA-1, ALPHA-4/BETA-1, ALPHA-5/BETA-1, ALPHA-8/BETA-1, ALPHA-
 10/BETA-1, ALPHA-11/BETA-1 AND ALPHA-V/BETA-1 ARE RECEPTORS FOR
 FIBRONECTIN. ALPHA-4/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN
 THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF FIBRONECTIN.
 CC INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRINOGEN. INTEGRIN
 CC ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-6/BETA-1 AND ALPHA-7/BETA-1
 ARE RECEPTORS FOR LAMININ. INTEGRIN ALPHA-4/BETA-1 IS A RECEPTOR
 FOR VCAM1. IT RECOGNIZES THE SEQUENCE Q-I-D-S IN VCAM1. INTEGRIN
 CC ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOTACTIN AND
 CC OSTOPONTIN. IT RECOGNIZES THE SEQUENCE A-E-I-D-G-I-E-L IN
 CC CYTOTACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPLIGRIN
 CC AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR
 CC VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A
 CC WIDE ARRAY OF LIGANDS. ISOFORM BETA-1B INTERFERES WITH ISOFORM
 CC BETA-1A RESULTING IN A DOMINANT NEGATIVE EFFECT ON CELL ADHESION
 CC AND MIGRATION (IN VITRO).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-1
 CC ASSOCIATES WITH EITHER ALPHA-1, ALPHA-2, ALPHA-3, ALPHA-4, ALPHA-
 CC 5, ALPHA-6, ALPHA-7, ALPHA-8, ALPHA-9, ALPHA-10, ALPHA-11 OR
 CC ALPHA-V.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ISOFORM BETA-1B
 CC DOES NOT LOCALIZE TO FOCAL ADHESIONS.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; BETA-1A (SHOWN HERE), BETA-1B,
 CC BETA-1C, BETA-1C-2 AND BETA-1D; ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM BETA-1A IS WIDELY EXPRESSED, OTHER
 CC ISOFORMS ARE GENERALLY COEXPRESSED WITH A MORE RESTRICTED
 CC DISTRIBUTION. ISOFORM BETA-1B IS EXPRESSED IN SKIN, LIVER,
 CC SKELETAL MUSCLE, CARDIAC MUSCLE, PLACENTA, UMBILICAL VEIN
 CC ENDOTHELIAL CELLS, NEUROBLASTOMA CELLS, LYMPHOMA CELLS, HEPATOMA
 CC CELLS AND ASTROCYTOMA CELLS. ISOFORMS BETA-1C AND BETA-1C-2 ARE
 CC EXPRESSED IN MUSCLE, KIDNEY, LIVER, PLACENTA, CERVICAL EPITHELIUM,
 CC UMBILICAL VEIN ENDOTHELIAL CELLS, FIBROBLAST CELLS, EMBRYONAL
 CC KIDNEY CELLS, PLATELETS AND SEVERAL BLOOD CELL LINES. ISOFORM
 CC BETA-1C-2, RATHER THAN ISOFORM BETA-1C, IS SELECTIVELY EXPRESSED IN
 CC PRIMARY T-CELLS. ISOFORM BETA-1C IS EXPRESSED IN NONPROLIFERATING
 CC AND DIFFERENTIATED PROSTATE GLAND EPITHELIAL CELLS. ISOFORM BETA-
 CC 1D IS EXPRESSED SPECIFICALLY IN STRIATED MUSCLE (SKELETAL AND
 CC CARDIAC MUSCLE).
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 VNFA-LIKE DOMAIN.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD29 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd29.htm".
 CC -----
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```

CC EMBL: X07979; CAA30790.1; -
DR EMBL: U33882; AAA79835.1; -
DR EMBL: U33875; AAA79835.1; JOINED.
DR EMBL: M84237; AAA74402.1; -
DR EMBL: U33879; AAA79832.1; -
DR EMBL: M34189; AAA59182.1; -
DR EMBL: U33880; AAA79833.1; -
DR EMBL: U33879; AAA79833.1; JOINED.
DR EMBL: U28252; AAA81366.1; -
DR EMBL: U33882; AAA79834.1; -
DR EMBL: U33879; AAA79834.1; JOINED.
DR EMBL: U33881; AAA79834.1; JOINED.
DR EMBL: M84237; AAA74403.1; -
DR PIR: B27079; B27079.
DR Genew: HGNC:6153; ITGB1.
DR MIM: 135630; -
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002369; Integrin_B.
DR InterPro: IPR001169; Integrin_beta_C.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF00362; Integrin_B.
DR PRINTS: PR01186; INTEGRINB.
DR PRODOM: PD001811; Integrin_B; 1.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00187; INB; 1.
DR SMART: SM00423; PSI; 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS00243; INTEGRIN_BETA; 3.
DR PROSITE: PS00042; EGF_1; UNKNOWN_2.
KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW Repeat; Signal; Phosphorylation; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 798 INTEGRIN BETA-1.
FT DOMAIN 21 728 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 729 751 POTENTIAL.
FT DOMAIN 752 798 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 140 378 VWA-LIKE.
FT DOMAIN 466 635 4 CYSTEINE-RICH TANDEM REPEATS.
FT REPEAT 466 515 I.
FT REPEAT 516 559 II.
FT REPEAT 560 598 III.
FT REPEAT 599 635 IV.
FT DISULFID 27 464 BY SIMILARITY.
FT DISULFID 35 45 BY SIMILARITY.
FT DISULFID 38 75 BY SIMILARITY.
FT DISULFID 207 213 BY SIMILARITY.
FT DISULFID 261 301 BY SIMILARITY.
FT DISULFID 401 415 BY SIMILARITY.
FT DISULFID 435 691 BY SIMILARITY.
FT DISULFID 462 466 BY SIMILARITY.
FT DISULFID 477 489 BY SIMILARITY.
FT DISULFID 486 525 BY SIMILARITY.
FT DISULFID 491 500 BY SIMILARITY.
FT DISULFID 502 516 BY SIMILARITY.
FT DISULFID 531 536 BY SIMILARITY.
FT DISULFID 533 568 BY SIMILARITY.
FT DISULFID 538 553 BY SIMILARITY.
FT DISULFID 555 560 BY SIMILARITY.
FT DISULFID 574 579 BY SIMILARITY.
FT DISULFID 576 607 BY SIMILARITY.
FT DISULFID 581 590 BY SIMILARITY.
FT DISULFID 592 599 BY SIMILARITY.
FT DISULFID 613 618 BY SIMILARITY.

Query Match 69.5%; Score 41; DB 1; Length 798;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPQ 9
|||||||

DB 122 RLRSGEPQ 129

RESULT 3
RNK6_AOTTR STANDARD; PRT; 150 AA.
AC O46528;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
GN RNASE6.
OS Aotus trivirgatus (Night monkey) (Douroucouli).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotus.
OC NCBI_TaxID=9505;
RX MEDLINE=98311672; PubMed=9647635;
RA Deming M.S., Dyer K.D., Bankier A.T., Piper M.B., Dear P.H.,
RA Rosenberg H.F.;
RT "Ribonuclease k6: chromosomal mapping and divergent rates of
RT evolution within the RNase A gene superfamily.";
RL Genome Res. 8:599-607(1998).
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC EMBL: AF037084; AAB94746.1; -
DR HSP: P00656; ISSA.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Signal; Glycoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 150 RIBONUCLEASE K6.
FT ACT_SITE 38 61 BY SIMILARITY.
FT ACT_SITE 61 61 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 46 104 BY SIMILARITY.
FT DISULFID 60 114 BY SIMILARITY.
FT DISULFID 78 129 BY SIMILARITY.
FT DISULFID 85 92 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 150 AA; 17034 MW; C20D36C673C1A495 CRC64;

Query Match 65.3%; Score 38.5; DB 1; Length 150;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSGE-PQC 10
|||||

DB 104 CRLTSGKYPQC 114

RESULT 4
RNK6_CERAE STANDARD; PRT; 150 AA.
AC O46534;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

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DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
GN RNASE6.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98311672; PubMed=9647635;
RA Deming M.S., Dyer K.D., Bankier A.T., Piper M.B., Dear P.H.,
RA Rosenberg H.F.;
RT "Ribonuclease K6: chromosomal mapping and divergent rates of
RT evolution within the RNase A gene superfamily.";
RL Genome Res. 8:599-607(1998).
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF037090; AAB94752.1;
CC HSP; P00656; ILSO.
CC InterPro: IPR001427; RNaseA.
CC Pfam: PF00074; rnaseA; 1.
CC PRINTS: PR00794; RIBONUCLEASE.
CC ProDom: PD000535; RNaseA; 1.
CC SMART; SM00092; RNase_Pc; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC Hydroxylase; Nuclease; Endonuclease; Signal; Glycoprotein.
CC SIGNAL 1 23 BY SIMILARITY.
CC CHAIN 24 150 RIBONUCLEASE K6.
CC ACT_SITE 38 38 BY SIMILARITY.
CC ACT_SITE 61 61 BY SIMILARITY.
CC ACT_SITE 145 145 BY SIMILARITY.
CC DISULFID 46 104 BY SIMILARITY.
CC DISULFID 60 114 BY SIMILARITY.
CC DISULFID 78 129 BY SIMILARITY.
CC DISULFID 85 92 BY SIMILARITY.
CC CARBOHYD 55 55 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 150 AA; 17178 MW; 0424428106EB8E07 CRC64;
CC
CC Query Match 65.3%; Score 38.5; DB 1; Length 150;
CC Best Local Similarity 72.7%; Pred. No. 2.5;
CC Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 CRLRSGE-PQC 10
DB 104 CRTSGKYPQC 114
DB
RESULT 5
RNK6_GORGO
ID RNK6_GORGO STANDARD; PRT; 150 AA.
AC O46532;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
GN RNASE6.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=98311672; PubMed=9647635;
RA Deming M.S., Dyer K.D., Bankier A.T., Piper M.B., Dear P.H.,
RA Rosenberg H.F.;
RT "Ribonuclease K6: chromosomal mapping and divergent rates of
RT evolution within the RNase A gene superfamily.";
RL Genome Res. 8:599-607(1998).
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC
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CC
CC EMBL; AF037088; AAB94750.1;
CC HSP; P00656; ILSO.
CC InterPro: IPR001427; RNaseA.
CC Pfam: PF00074; rnaseA; 1.
CC PRINTS: PR00794; RIBONUCLEASE.
CC ProDom: PD000535; RNaseA; 1.
CC SMART; SM00092; RNase_Pc; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC Hydroxylase; Nuclease; Endonuclease; Signal; Glycoprotein.
CC SIGNAL 1 23 BY SIMILARITY.
CC CHAIN 24 150 RIBONUCLEASE K6.
CC ACT_SITE 38 38 BY SIMILARITY.
CC ACT_SITE 61 61 BY SIMILARITY.
CC ACT_SITE 145 145 BY SIMILARITY.
CC DISULFID 46 104 BY SIMILARITY.
CC DISULFID 60 114 BY SIMILARITY.
CC DISULFID 78 129 BY SIMILARITY.
CC DISULFID 85 92 BY SIMILARITY.
CC CARBOHYD 55 55 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 150 AA; 17222 MW; D33EA034CD487E71 CRC64;
CC
CC Query Match 65.3%; Score 38.5; DB 1; Length 150;
CC Best Local Similarity 72.7%; Pred. No. 2.5;
CC Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 CRLRSGE-PQC 10
DB 104 CRTSGKYPQC 114
DB
RESULT 6
RNK6_HUMAN
ID RNK6_HUMAN STANDARD; PRT; 150 AA.
AC Q93091;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
GN RNASE6 OR RNS6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96433147; PubMed=8836175;
RA Rosenberg H.F., Dyer K.D.;
RT "Molecular cloning and characterization of a novel human ribonuclease
RT (RNase K6): increasing diversity in the enlarging ribonuclease gene
RT family.";
RL Nucleic Acids Res. 24:3507-3513(1996).
RN [2]
RP REVISION TO 76.
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RA Rosenberg H.F.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: STRONG EXPRESSION IN LUNG, FOLLOWED BY HEART,
CC PLACENTA, KIDNEY, PANCREAS, LIVER, BRAIN AND SKELETAL MUSCLE. ALSO
CC EXPRESSED IN MONOCYTES AND NEUTROPHILS.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC -----
CC EMBL; U64998; AAC51848.1;
CC HSSP; P00656; ILISO.
CC Genew; HGNC:10048; RNASEB6.
CC MIM; 601981;
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; rnasea; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNaseA; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC HydroLase; Nuclease; Endonuclease; Signal; Glycoprotein; Polymorphism.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 150 RIBONUCLEASE K6.
FT ACT_SITE 38 38 BY SIMILARITY.
FT ACT_SITE 61 61 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 46 104 BY SIMILARITY.
FT DISULFID 60 114 BY SIMILARITY.
FT DISULFID 78 129 BY SIMILARITY.
FT DISULFID 85 92 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARIANT 89 89 R -> Q (IN DBSNP:1045922).
FT /FTID=VAR_012048.
SQ SEQUENCE 150 AA; 17196 MW; 4C1F722066BCC13A CRC64;

Query Match 65.3%; Score 38.5; DB 1; Length 150;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSCE-PQC 10
DB 104 CRLTSKYPQC 114

RESULT 7
RNK6_MACMU
ID RNK6_MACMU STANDARD; PRT; 150 AA.
AC O46533;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
GN RNASEB6.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX DEMING M.S., DYER K.D., BANKIER A.T., PIPER M.B., DEAR P.H.,
RA ROSENBERG H.F.;
RL Evolution within the RNase A gene superfamily.";
RT "Ribonuclease K6: chromosomal mapping and divergent rates of
evolution within the RNase A gene superfamily.";
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC -----
CC EMBL; U64998; AAC51848.1;
CC HSSP; P00656; ILISO.
CC Genew; HGNC:10048; RNASEB6.
CC MIM; 601981;
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; rnasea; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNaseA; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC HydroLase; Nuclease; Endonuclease; Signal; Glycoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 150 RIBONUCLEASE K6.
FT ACT_SITE 38 38 BY SIMILARITY.
FT ACT_SITE 61 61 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 46 104 BY SIMILARITY.
FT DISULFID 60 114 BY SIMILARITY.
FT DISULFID 78 129 BY SIMILARITY.
FT DISULFID 85 92 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARIANT 89 89 R -> Q (IN DBSNP:1045922).
FT /FTID=VAR_012048.
SQ SEQUENCE 150 AA; 17196 MW; 4C1F722066BCC13A CRC64;

Query Match 65.3%; Score 38.5; DB 1; Length 150;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSCE-PQC 10
DB 104 CRLTSKYPQC 114

RESULT 8
RNK6_MIOTA
ID RNK6_MIOTA STANDARD; PRT; 150 AA.
AC O46531;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
GN RNASE6.
OS Miopithecus talapoin (Talapoin) (Cercopithecus talapoin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Miopithecus.
OX NCBI_TaxID=36231;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98311672; PubMed=9647635;
RX DENING M.S., DYER K.D., BANKIER A.T., PIPER M.B., DEAR P.H.,
RA ROSENBERG H.F.;
RL "Ribonuclease K6: chromosomal mapping and divergent rates of
evolution within the RNase A gene superfamily.";
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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CC -----
CC EMBL; AF037089; AAB94751.1;
CC HSSP; P00656; ILISO.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; rnasea; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNaseA; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC HydroLase; Nuclease; Endonuclease; Signal; Glycoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 150 RIBONUCLEASE K6.
FT ACT_SITE 38 38 BY SIMILARITY.
FT ACT_SITE 61 61 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 46 104 BY SIMILARITY.
FT DISULFID 60 114 BY SIMILARITY.
FT DISULFID 78 129 BY SIMILARITY.
FT DISULFID 85 92 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 150 AA; 17177 MW; 3144428106F759BB CRC64;

Query Match 65.3%; Score 38.5; DB 1; Length 150;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSCE-PQC 10
DB 104 CRLTSKYPQC 114

```


FT ACT_SITE 61 61 BY SIMILARITY.
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT DISULFID 46 104 BY SIMILARITY.
 FT DISULFID 60 114 BY SIMILARITY.
 FT DISULFID 78 129 BY SIMILARITY.
 FT DISULFID 85 92 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 150 AA; 17237 MW; 463299F106F759AA CRC64;

Query Match 65.3%; Score 38.5; DB 1; Length 150;
 Best Local Similarity 72.7%; Pred. No. 2.5;
 Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSGE-POC 10
 DB 104 CRLTSGKYPC 114

RESULT 11

RNK6_SAGOE
 ID RNK6_SAGOE STANDARD; PRT; 150 AA.
 AC O46530;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
 GN RNASE6.
 OS *Saguinus oedipus* (Cotton-top tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=9430;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98311672; PubMed=9647635;
 RA Deming M.S., Dyer K.D., Bankier A.T., Piper M.B., Dear P.H.,
 RA Rosenberg H.F.;
 RT "Ribonuclease K6: chromosomal mapping and divergent rates of
 evolution within the RNase A gene superfamily.";
 RL Genome Res. 8:599-607(1998).
 CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF037086; AAB94748.1; -.
 CC HSSP; P00656; 1SSA.
 CC InterPro; IPR001427; RNaseA.
 CC Pfam; PF00074; rnaase; 1.
 CC PRINTS; PR00794; RIBONUCLEASE.
 CC ProDom; PD000535; RNaseA; 1.
 CC SMART; SM00092; RNasePc; 1.
 CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolase; Nuclease; Endonuclease; Signal; Glycoprotein.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 150 RIBONUCLEASE K6.
 FT ACT_SITE 38 38 BY SIMILARITY.
 FT ACT_SITE 61 61 BY SIMILARITY.
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT DISULFID 46 104 BY SIMILARITY.
 FT DISULFID 60 114 BY SIMILARITY.
 FT DISULFID 78 129 BY SIMILARITY.
 FT DISULFID 85 92 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 150 AA; 17044 MW; 8B6AACAA8FAF93 CRC64;

Query Match 65.3%; Score 38.5; DB 1; Length 150;
 Best Local Similarity 72.7%; Pred. No. 2.5;
 Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSGE-POC 10
 DB 104 CRLTSGKYPC 114

RESULT 12

URTG_DESRO
 ID URTG_DESRO STANDARD; PRT; 394 AA.
 AC P49150;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA
 DE gamma).
 DE gamma).
 OS *Desmodus rotundus* (Vampire bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Chiroptera; Microchiroptera; Phyllostomidae;
 OC Desmodontinae; Desmodus.
 OX NCBI_TaxID=9430;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RX MEDLINE=92039036; PubMed=1937019;
 RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 RA Alagon A., Donner P., Schleuning W.D.;
 RT "The plasminogen activator family from the salivary gland of the
 RT vampire bat *Desmodus rotundus*: cloning and expression.";
 RL Gene 105:229-237(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=93393059; PubMed=1309059;
 RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
 RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 RA Donner P.;
 RT "Plasminogen activators from the saliva of *Desmodus rotundus* (common
 RT vampire bat): unique fibrin specificity.";
 RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
 CC -!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS
 CC EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
 CC AGENT.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-I-Val bond in
 CC plasminogen to form plasmin.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M63990; AAA31595.1; -.
 CC HSSP; P98119; IAS1.
 CC MEROPS; S01.239; -.
 CC InterPro; IPR001314; Chymotrypsin.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR001254; Ser_protease_Try.
 CC Pfam; PF00051; kringle; 1.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00018; KRINGLE.
 CC ProDom; PD000395; Kringle; 1.
 CC SMART; SM00130; KR; 1.
 CC SMART; SM00020; Tryp-Spc; 1.
 CC PROSITE; PS00021; KRINGLE_1; 1.

DR PROSITE: PS50070; KRINGLE_2; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KRingle; Signal; Multigene family.
 FT SIGNAL 1 36
 FT CHAIN 37 394
 FT DOMAIN 45 126
 FT DOMAIN 142 394
 FT ACT_SITE 189 189
 FT ACT_SITE 238 238
 FT ACT_SITE 345 345
 FT ACT_SITE 345 345
 FT DISULFID 45 126
 FT DISULFID 66 108
 FT DISULFID 97 121
 FT DISULFID 131 262
 FT DISULFID 174 190
 FT DISULFID 182 251
 FT DISULFID 276 351
 FT DISULFID 308 324
 FT DISULFID 341 369
 FT CARBOHYD 315 315
 SQ SEQUENCE 394 AA; 44105 MW; 9CCD6F5F3D81FCD CRC64;
 Query Match 64.4%; Score 38; DB 1; Length 394;
 Best Local Similarity 66.7%; Pred. No. 8.4;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RLRSGEPOC 10
 DB 243 QLKSGSPQC 251
 RESULT 13
 ID URTB_DESRO STANDARD; PRT; 431 AA.
 AC P98121;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSFA beta)
 OS Desmodus rotundus (Vampire bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
 OC Desmodontinae; Desmodus.
 OX NCBI_TaxID=9430;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RX MEDLINE=9203036; PubMed=1937019;
 RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 Alaon A., Donner P., Schleuning W.D.;
 FT "The plasminogen activator family from the salivary gland of the
 FT vampire bat Desmodus rotundus: cloning and expression.";
 RL Gene 105:229-237(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=93393059; PubMed=1309059;
 RA Schleuning W.-D., Alaon A., Boidol W., Bringmann P., Petri T.,
 RA Kraetzschmar J., Haendler B., Langer G., Baidus B., Witt W.,
 Donner P.;
 RT "Plasminogen activators from the saliva of Desmodus rotundus (common
 RT vampire bat): unique fibrin specificity.";
 RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
 CC -!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS
 CC EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
 CC AGENT.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M63989; AAA31594.1; -
 DR HSPSP; P98119; IASI.
 DR MEROPS; S01.239; -
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; EGF-like domain; Signal; Multigene family.
 FT SIGNAL 1 36
 FT CHAIN 37 431
 FT DOMAIN 37 75
 FT DOMAIN 82 163
 FT DOMAIN 179 431
 FT ACT_SITE 226 226
 FT ACT_SITE 275 275
 FT ACT_SITE 382 382
 FT DISULFID 41 52
 FT DISULFID 46 63
 FT DISULFID 65 74
 FT DISULFID 82 163
 FT DISULFID 103 145
 FT DISULFID 134 158
 FT DISULFID 168 299
 FT DISULFID 211 227
 FT DISULFID 219 288
 FT DISULFID 313 388
 FT DISULFID 345 361
 FT DISULFID 378 406
 FT CARBOHYD 139 139
 FT CARBOHYD 352 352
 SQ SEQUENCE 431 AA; 48221 MW; 699B5E675B162CBF CRC64;
 Query Match 64.4%; Score 38; DB 1; Length 431;
 Best Local Similarity 66.7%; Pred. No. 9.2;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RLRSGEPOC 10
 DB 280 QLKSGSPQC 288
 RESULT 14
 ID URT2_DESRO STANDARD; PRT; 477 AA.
 AC P15638;

DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Salivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA
DE alpha-2) (BAT-PA) (T-plasminogen activator).
OS Desmodus rotundus (Vampire bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
OC Desmodontinae; Desmodus.
OX NCBI_TaxID=9430;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=92039036; PubMed=1937019;
RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
RA Alagon A., Donner P., Schleuning W.D.;
RT "The plasminogen activator family from the salivary gland of the
RT vampire bat Desmodus rotundus: cloning and expression.";
RL Gene 105:229-237(1991).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Salivary gland;
RX MEDLINE=90036867; PubMed=2509450;
RA Gardell S.J., Duong L.T., Diehl R.E., York J.D., Hare T.R.,
RA Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;
RT "Isolation, characterization, and cDNA cloning of a vampire bat
RT salivary plasminogen activator.";
RL J. Biol. Chem. 264:17947-17952(1989).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=93393059; PubMed=1309059;
RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
RA Donner P.;
RT "Plasminogen activators from the saliva of Desmodus rotundus (common
RT vampire bat): unique fibrin specificity.";
RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
CC -!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS
CC EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
CC AGENT.
CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-I-Val bond in
CC plasminogen to form plasmin.
CC -!- ENZYME REGULATION: ACTIVITY TOWARD PLASMINOGEN IS STIMULATED IN
CC THE PRESENCE OF FIBRIN I.
CC -!- DOMAIN: THE FIBRONECTIN TYPE-I DOMAIN MEDIATES BINDING TO FIBRIN,
CC AND THE KRINGLE DOMAIN APPARENTLY MEDIATES FIBRIN-INDUCED
CC STIMULATION OF ACTIVITY.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE I DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
CC -----
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CC -----
DR EMBL; M63988; AAA31593.1; -;
DR EMBL; J05082; AAA31596.1; -;
DR PIR; A34369; A34369.
DR HSP; P98119; 1A51.
DR MEROPS; S01.232; -;
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000083; Fibrinctn1.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00039; fn1; 1.

DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Signal; Multigene family.
FT SIGNAL 1 36
FT CHAIN 37 477
FT DOMAIN 40 82
FT DOMAIN 83 121
FT DOMAIN 128 209
FT DOMAIN 225 477
FT ACT_SITE 272 272
FT ACT_SITE 321 321
FT ACT_SITE 428 428
FT DISULFID 42 72
FT DISULFID 70 79
FT DISULFID 87 98
FT DISULFID 92 109
FT DISULFID 111 120
FT DISULFID 128 209
FT DISULFID 149 191
FT DISULFID 180 204
FT DISULFID 214 345
FT DISULFID 257 273
FT DISULFID 265 334
FT DISULFID 359 434
FT DISULFID 391 407
FT DISULFID 424 452
FT CARBOHYD 185 185
FT CARBOHYD 398 398
FT CONFLICT 403 403
FT CONFLICT 417 417
FT CONFLICT 435 435
SQ SEQUENCE 477 AA; 53719 MW; 17486555C0E5077C CRC64;
Query Match 64.4%; Score 38; DB 1; Length 477;
Best Local Similarity 66.7%; Pred No. 10;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 RLRSGEPC 10
Db 326 QLKSGSPQC 334
RESULT 15
Y0AA_ECOLI
ID Y0AA_ECOLI STANDARD; PRT; 636 AA.
AC P76257; O07973;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ATP-dependent helicase yoaA.
GN Y0AA OR B1808.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasubraman S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -!- SIMILARITY: BELONGS TO THE HELICASE FAMILY. DING SUBFAMILY.
CC STRONG, TO H.INFLUENZAE HI0387.
CC -----
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CC -----
DR EMBL; AE000275; AAC74878.1; -
DR EMBL; D90824; BAAL5612.1; -
DR EMBL; D90825; BAAL5617.1; -
DR EcoGene; EG13513; yoaA.
KW Hypothetical protein; Hydrolase; Helicase; ATP-binding;
KW DNA-binding; Complete proteome.
FT NP_BIND 45 52 ATP (POTENTIAL).
FT SITE 225 228 DEAH BOX.
FT DOMAIN 193 196 POLY-VAL.
SQ SEQUENCE 636 AA; 70377 MW; 14CEBD04CCBE701F CRC64;

Query Match 64.4%; Score 38; DB 1; Length 636;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRLRSGEP 8
DB 557 CRLRGDP 564
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|
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|

Search completed: January 30, 2003, 13:32:17
Job time : 13 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 30, 2003, 13:32:01 ; Search time 29 seconds
(without alignments)
71.051 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLRGEPQC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	45	76.3	3767	5 Q9UAI3	Q9ual3 caenorhabdi
2	42	71.2	86	16 Q9K0E9	Q9k0e9 neisseria m
3	42	71.2	2091	5 Q9VJ69	Q9vj69 drosophila
4	41	69.5	798	4 Q8WUM6	Q8wum6 homo sapien
5	40	67.8	892	5 P91085	P91085 caenorhabdi
6	39	66.1	55	16 Q9RKI7	Q9rki7 streptomyce
7	39	66.1	66	5 Q9NL69	Q9nl69 caenorhabdi
8	39	66.1	85	5 Q9NL71	Q9nl71 caenorhabdi
9	39	66.1	205	4 Q9V4U5	Q9v4u5 homo sapien
10	39	66.1	285	13 Q8QFQ2	Q8qfq2 xenopus lae
11	38.5	65.3	127	6 Q9TV27	Q9tv27 nysticebus
12	38	64.4	114	4 Q05835	Q05835 homo sapien
13	38	64.4	157	5 Q9V9A1	Q9v9a1 drosophila
14	38	64.4	368	10 Q9XFB9	Q9xfb9 arabidopsis
15	38	64.4	423	4 Q9BPW2	Q9bpw2 homo sapien
16	38	64.4	435	4 Q9BZX8	Q9bzx8 homo sapien

17	38	64.4	560	4 Q9BZY0	Q9bzy0 homo sapien
18	38	64.4	585	4 Q9BZX6	Q9bzx6 homo sapien
19	38	64.4	611	4 Q9BZY3	Q9bzy3 homo sapien
20	38	64.4	633	4 Q9BZX9	Q9bzx9 homo sapien
21	38	64.4	634	16 Q8ZET2	Q8zet2 versinia pe
22	38	64.4	636	16 Q8XF32	Q8xf32 salmonella
23	38	64.4	636	16 Q8XDR3	Q8xdr3 escherichia
24	38	64.4	641	4 Q15959	Q15959 homo sapien
25	38	64.4	646	16 Q9KQK8	Q9kqk8 vibrio chol
26	38	64.4	706	13 Q42593	Q42593 xenopus lae
27	38	64.4	759	4 Q9BWP7	Q9bwp7 homo sapien
28	38	64.4	781	4 Q8WUA0	Q8wua0 homo sapien
29	38	64.4	797	4 Q15156	Q15156 homo sapien
30	38	64.4	824	4 Q9BZY2	Q9bzy2 homo sapien
31	38	64.4	829	4 Q9BZX7	Q9bzx7 homo sapien
32	38	64.4	854	4 Q9BZY1	Q9bzy1 homo sapien
33	37.5	63.6	127	6 Q9TV26	Q9tv26 eulemur ful
34	37.5	63.6	1515	13 Q9DE37	Q9de37 brachydanio
35	37	62.7	161	17 Q58640	Q58640 pyrococcus
36	37	62.7	182	2 Q46616	Q46616 erwinia amy
37	37	62.7	234	4 Q96IU2	Q96iu2 homo sapien
38	37	62.7	263	4 Q95633	Q95633 homo sapien
39	37	62.7	337	5 Q9VL33	Q9vl33 drosophila
40	37	62.7	484	5 Q22967	Q22967 caenorhabdi
41	37	62.7	537	10 Q9AY52	Q9ay52 oryza sativ
42	37	62.7	553	11 P97543	P97543 rattus norv
43	37	62.7	793	4 Q9H522	Q9h522 homo sapien
44	37	62.7	798	6 Q9GLP0	Q9glp0 sus scrofa
45	37	62.7	798	6 Q8SQC0	Q8sqc0 bos taurus

ALIGNMENTS

RESULT 1

Q9UAI3	ID	Q9UAI3	PRELIMINARY;	PRT; 3767 AA.
AC	Q9UAI3	Q21340;		
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Transmembrane cell adhesion receptor MUA-3 precursor (K08E5.3 protein)			
DE	(Fragment)			
GN	MUA-3 OR K08E5.3.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peloderinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=N2;			
RA	Lu Z., Vogel B., Hedgecock E.;			
RT	"mua-3 mRNA Splicing Pattern Revealed."			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Kershaw J.K.;			
RN	Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-99069613; PubMed-9851916;			
RA	none;			
RT	"Genome sequence of the nematode C.elegans: A platform for			
RT	investigating biology."			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Berkis M., Smith A., Lloyd C.R.;			
RL	Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF139060; AAD29428.1; -			
DR	EMBL; Z30974; CAA83226.2; -			
DR	EMBL; Z30423; CAA83226.2; JOINED.			
DR	EMBL; Z30423; CAC42345.1; -			

DR EMBL; 230974; CAC42345.1; JOINED.
 DR HSP; P01130; ILDL.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR002172; LDL_recept_A.
 DR InterPro: IPR000082; SEA_domain.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam: PF00008; EGF_33.
 DR Pfam: PF00057; ldl_recept_a; 3.
 DR Pfam: PF01390; SEA; 2.
 DR Pfam: PF00092; vwa; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR PRINTS; PR00261; LDLRECEPTOR.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 45.
 DR SMART; SM00192; LDLA; 4.
 DR SMART; SM00200; SEA; 2.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00010; ASX-HYDROXYL; UNKNOWN_32.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 6.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00068; LDLRA_2; 2.
 DR PROSITE; PS50024; SEA; 4.
 DR PROSITE; PS50234; VWEA; 2.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Receptor; Repeat;
 KW Signal.
 FT SIGNAL. 1 24 POTENTIAL.
 FT CHAIN 25 >3767 3.
 FT FT
 FT NON_TER 3767 3767
 FT SEQUENCE 3767 AA; 417284 MW; 8D3A3AE5EA50AEB8E CRC64;
 Query Match 76.38; Score 45; DB 5; Length 3767;
 Best Local Similarity 70.08; Pred. No. 9;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRLRSGEPQC 10
 DB 2088 CRLMGGEPC 2097
 ID Q9K0E9 PRELIMINARY; PRT; 86 AA.
 AC Q9K0E9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein NMB0658.
 GN NMB0658.
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
 RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 RA Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 RT MC58.";
 RT Science 287:1809-1815(2000).
 DR EMBL; AE002420; AAF62315.1; -.
 DR FMBL; AE002420; AAF62315.1; -.

DR TIGR; NMB0658; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 86 AA; 9933 MW; 5CEB3DF0A5F8D0E5 CRC64;
 Query Match 71.2%; Score 42; DB 16; Length 86;
 Best Local Similarity 66.7%; Pred. No. 0.83;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;
 QY 1 CRLR--SGEPQC 10
 DB 24 CRLRMSTGGPQC 35
 ID Q9VJ69 PRELIMINARY; PRT; 2091 AA.
 AC Q9VJ69;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE CG15165 protein.
 GN CG15165
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Cocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Slen T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 RL EMBL; AF003659; AAF53685.1; -.
 DR FlyBase; FBgn0032695; CG15165.
 SQ SEQUENCE 2091 AA; 241956 MW; 63AA3D744205AE14 CRC64;

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Query Match          71.2%; Score 42; DB 5; Length 2091;
Best Local Similarity 88.9%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
DB 1632 CRLRSGEAQ 1640

RESULT 4
Q8WUM6 PRELIMINARY; PRT; 798 AA.
AC Q8WUM6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 88.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020057; AAH20057.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002369; Integrin_B.
DR InterPro; IPR001169; Integrin_beta_C.
DR InterPro; IPR003659; Plexin-like.
DR Pfam; PF00362; Integrin_B.1.
DR PRINTS; PR01186; INTEGRINB.
DR ProDom; PD001811; Integrin_B.1.
DR SMART; SM00187; INB; 1.
DR SMART; SM00423; PSI; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS00243; INTEGRIN_BETA; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 798 AA; 88415 MW; DE35979C1625578C CRC64;

Query Match          69.5%; Score 41; DB 4; Length 798;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPO 9
DB 122 RLRSGEPO 129

RESULT 5
P91085 PRELIMINARY; PRT; 892 AA.
AC P91085;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 99.7 kDa protein.
GN F55A12.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None.
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=BRISTOL N2;
RA Pauley A., Gattung S.;
RT "The sequence of C. elegans cosmid F55A12.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003130; AAB54129.1; -.
DR InterPro; IPR003100; PAZ.
DR InterPro; IPR003165; P1wi.
DR Pfam; PF02170; PAZ; 1.
DR Pfam; PF02171; P1wi; 1.
KW Hypothetical protein.
SQ SEQUENCE 892 AA; 99749 MW; 44FE58335244DE3E CRC64;

Query Match          67.8%; Score 40; DB 5; Length 892;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPOC 10
DB 511 CRFSSGDPPC 520

RESULT 6
Q9RK17 PRELIMINARY; PRT; 55 AA.
AC Q9RK17;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein SC03445.
GN SC03445 OR SCE46.02C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)";
RL Nature 417:141-147(2002).
DR EMBL; AL133252; CAB61853.1; -.
KW Hypothetical protein.
SQ SEQUENCE 55 AA; 5927 MW; BF89F887A528D263 CRC64;

Query Match          66.1%; Score 39; DB 16; Length 55;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPOC 10
DB 4 CLARSGFPQC 13

RESULT 7
Q9NL69 PRELIMINARY; PRT; 66 AA.
AC Q9NL69;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

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DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE ABF-2 (Fragment).
 GN ABF-2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kato Y.;
 RT "a polycistronic precursor RNA for abf operon in Caenorhabditis
 RT elegans.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB029811; BAA89492.1; -;
 FT NON_TER 66
 SQ SEQUENCE 66 AA; 7017 MW; E845F5F753FAA689 CRC64;
 Query Match 66.1%; Score 39; DB 5; Length 66;
 Best Local Similarity 60.0%; Pred. No. 2.5;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CRLRSGEPOC 10
 Db 55 CKKRSGRPTC 64
 RESULT 8
 Q9NL71
 ID Q9NL71 PRELIMINARY; PRT; 85 AA.
 AC Q9NL71;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE ABF-2 precursor (Hypothetical 8.9 kDa protein).
 GN ABF-2 OR C50F2.10.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kato Y.;
 RT "ABF-2, an ASABF-type antimicrobial peptide in Caenorhabditis
 RT elegans.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB029811; BAA89492.1; -;
 FT NON_TER 66
 SQ SEQUENCE 66 AA; 7017 MW; E845F5F753FAA689 CRC64;
 Query Match 66.1%; Score 39; DB 5; Length 66;
 Best Local Similarity 60.0%; Pred. No. 2.5;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CRLRSGEPOC 10
 Db 55 CKKRSGRPTC 64
 RESULT 9
 Q9Y4U5
 ID Q9Y4U5 PRELIMINARY; PRT; 205 AA.
 AC Q9Y4U5;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical 21.5 kDa protein (Fragment).
 GN DKFZP586I11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ottensvaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL050131; CAB43283.2; -;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 205 AA; 21548 MW; D88EB7A823C618E4 CRC64;
 Query Match 66.1%; Score 39; DB 4; Length 205;
 Best Local Similarity 75.0%; Pred. No. 7.7;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LRSGEPOC 10
 Db 170 LRAGDPOC 177
 RESULT 10
 Q8QFQ2
 ID Q8QFQ2 PRELIMINARY; PRT; 285 AA.
 AC Q8QFQ2;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Mig30.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ANTERIOR ENDOMESODERM OF THE SPEMANN ORGANIZER, AND ENDODERM;
 RX MEDLINE=21839545; PubMed=11850177;
 RA Hayata T., Tanegashima K., Takahashi S., Sogame A., Asashima M.;
 RT "Overexpression of the secreted factor Mig30 expressed in the Spemann
 RT organizer impairs morphogenetic movements during Xenopus
 RT gastrulation.";
 RL Mech. Dev. 112:37-51(2002).
 DR EMBL; AB035379; BAB84702.1; -;
 SQ SEQUENCE 285 AA; 31431 MW; 346295C6C77B6BE0 CRC64;
 Query Match 66.1%; Score 39; DB 13; Length 285;
 Best Local Similarity 57.1%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;
 QY 1 CRLRSQ----EPOC 10
 Db 92 CQLRGGHVNEPOC 105

Query Match 66.1%; Score 39; DB 5; Length 85;
 Best Local Similarity 60.0%; Pred. No. 3.2;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CRLRSGEPOC 10
 Db 55 CKKRSGRPTC 64
 RESULT 9
 Q9Y4U5
 ID Q9Y4U5 PRELIMINARY; PRT; 205 AA.
 AC Q9Y4U5;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical 21.5 kDa protein (Fragment).
 GN DKFZP586I11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ottensvaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL050131; CAB43283.2; -;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 205 AA; 21548 MW; D88EB7A823C618E4 CRC64;
 Query Match 66.1%; Score 39; DB 4; Length 205;
 Best Local Similarity 75.0%; Pred. No. 7.7;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LRSGEPOC 10
 Db 170 LRAGDPOC 177
 RESULT 10
 Q8QFQ2
 ID Q8QFQ2 PRELIMINARY; PRT; 285 AA.
 AC Q8QFQ2;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Mig30.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ANTERIOR ENDOMESODERM OF THE SPEMANN ORGANIZER, AND ENDODERM;
 RX MEDLINE=21839545; PubMed=11850177;
 RA Hayata T., Tanegashima K., Takahashi S., Sogame A., Asashima M.;
 RT "Overexpression of the secreted factor Mig30 expressed in the Spemann
 RT organizer impairs morphogenetic movements during Xenopus
 RT gastrulation.";
 RL Mech. Dev. 112:37-51(2002).
 DR EMBL; AB035379; BAB84702.1; -;
 SQ SEQUENCE 285 AA; 31431 MW; 346295C6C77B6BE0 CRC64;
 Query Match 66.1%; Score 39; DB 13; Length 285;
 Best Local Similarity 57.1%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;
 QY 1 CRLRSQ----EPOC 10
 Db 92 CQLRGGHVNEPOC 105

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RESULT 11
Q9TV27 ID Q9TV27 PRELIMINARY; PRT; 127 AA.
AC Q9TV27;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Ribonuclease k6 (Fragment)
OS Nycticebus coucang (slow loris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Loridae; Nycticebus.
OX NCBI_TaxID=9470;
RN [1]
RP SEQUENCE FROM N.A.
RA Deming M.S., Dyer K.D., Seekamp R.L., Rosenberg H.F.;
RT "Evolution of three primate ribonuclease genes: comparative analysis
RT of RNase 4, RNase k6, and RNase 2 (eosinophil-derived neurotoxin).";
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF078123; RAD48537.1; -
DR HSSP; P00656; 2RNS.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
FT NON_TER 1 127
FT SEQUENCE 127 AA; 14611 MW; 76F16ED9107DD66F CRC64;

Query Match 65.3%; Score 38.5; DB 6; Length 127;
Best Local Similarity 72.7%; Pred. No. 6;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSGE-PQC 10
DB 81 CRLTSKYPQC 91

RESULT 12
Q05835 ID Q05835 PRELIMINARY; PRT; 114 AA.
AC Q05835;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Promyelocytic leukemia protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93116464; PubMed=8380300;
RA Geng J.P., Tong J.H., Dong S., Wang Z.Y., Chen S.J., Chen Z.,
RA Zelen A., Berger R., Larsen C.J.;
RT "Localization of the chromosome 15 breakpoints and expression of
RT multiple PML-RAR alpha transcripts in acute promyelocytic leukemia: a
RT study of 28 Chinese patients.";
RL Leukemia 7:20-26(1993).
DR EMBL; S51489; AAD13865.1; -
DR NON_TER 1 114
DR SEQUENCE 114 AA; 12861 MW; 11E9933161535F8D CRC64;

Query Match 64.4%; Score 38; DB 4; Length 114;
Best Local Similarity 77.8%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGE-PQC 9
DB 53 CRLRQEPQ 61

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RESULT 13
Q9V9A1 ID Q9V9A1 PRELIMINARY; PRT; 157 AA.
AC Q9V9A1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CG15235 protein.
GN CG15235.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzby D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003790; AAF57395.1; -
DR FlyBase; FBgn0033103; CG15235.
DR InterPro; IPR000595; cNMP_binding.
DR Pfam; PF00027; cNMP_binding; 1.
DR PROSITE; PS50042; cNMP_BINDING_3; 1.
DR SEQUENCE 157 AA; 17664 MW; 46EBCB9F416D032B CRC64;

Query Match 64.4%; Score 38; DB 5; Length 157;
Best Local Similarity 70.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGE-PQC 10
DB 27 CRLRRVEPLC 36

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RESULT 14
Q9XFB9          PRELIMINARY;          PRT;    368 AA.
AC  Q9XFB9;
DT  01-NOV-1999 (TREMBLrel. 12, Created)
DT  01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT  01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE  Zinc finger protein 3.
GN  ZFN3
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX  NCBI_TaxID=3702;
[1]
RN  SEQUENCE FROM N.A.
RP  STRAIN=CV. COLOMBIA;
RC  Choi S., Lee J., Yi H., Shin B., Choi G.;
RT  "Characterization of zinc finger protein 3 (ZFN-3) in Arabidopsis
thaliana.";
RL  Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN=COLUMBIA;
RC  MEDLINE=97471969; PubMed=9330910;
RA  Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA  Miyajima N., Tabata S.;
RT  "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
features of the 1.6 Mb regions covered by twenty physically assigned
Pl clones.";
RL  DNA Res. 4:215-230(1997).
DR  ENBL; AF138872; AAD27875.1; -.
DR  ENBL; AB005242; BAB09623.1; -.
DR  InterPro; IPR000571; Znf_CCCCH.
DR  Pfam; PF00642; zf-CCCH; 5.
DR  SMART; SM00356; Znf_C3H1; 5.
SQ  SEQUENCE 368 AA; 40792 MW; 84EFCAAADB18A15C CRC64;

Query Match          64.4%; Score 38; DB 10; Length 368;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 CRLRSGEPQC 10
   I I I I I I I
Db  279 CVLSGSEPLC 288

RESULT 15
Q9BPW2          PRELIMINARY;          PRT;    423 AA.
AC  Q9BPW2;
DT  01-JUN-2001 (TREMBLrel. 17, Created)
DT  01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT  01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE  Tripartite motif protein TRIM19 iota (Tripartite motif protein TRIM19
etc.).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
[1]
RN  SEQUENCE FROM N.A.
RP  MEDLINE=92278759; PubMed=1594241;
RA  Fagioli M., Alcalay M., Pandolfi P.P., Venturini L., Mencarelli A.,
RA  Simeone A., Acampora D., Grignani F., Pelicci P.G.;
RT  "Alternative splicing of PML transcripts predicts coexpression of
several carboxy-terminally different protein isoforms.";
RL  Oncogene 7:1083-1091(1992).
[2]
RN  SEQUENCE FROM N.A.
RP  Reymond A., Meroni G.;
RT  "Deciphering the function of the Tripartite Motif containing

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proteins.";
RL  Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RA  Fagioli M., Reymond A., Meroni G.;
RL  Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN  [4]
RP  SEQUENCE FROM N.A.
RA  Reymond A., Meroni G.;
RT  "Deciphering the function of the Tripartite Motif containing
proteins.";
RL  Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC  -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR  ENBL; AF230409; AAG50188.1; -.
DR  ENBL; AF230407; AAG50186.1; -.
DR  HSP; P29590; IBOB.
DR  InterPro; IPR000315; Znf_Box.
DR  InterPro; IPR001841; Znf_ring.
DR  Pfam; PF00643; zf-B_box; 2.
DR  Pfam; PF00097; zf-C3HC4; 1.
DR  SMART; SM00336; BBOX; 1.
DR  SMART; SM00184; RING; 1.
DR  PROSITE; PS00518; ZF_RING_1; 1.
KW  Zinc-finger.
SQ  SEQUENCE 423 AA; 47574 MW; EE5031BE9C3B33C8 CRC64;

Query Match          64.4%; Score 38; DB 4; Length 423;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 CRLRSGEPQ 9
   I I I I I I I
Db  357 CRLRSEEPQ 365

Search completed: January 30, 2003, 13:34:19
Job time : 31 secs

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